

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2003, 00:12:01 ; Search time 236 Seconds

(Without alignments)
3463.879 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363
Sequence: 1 caggttaccctgaagaagc.....ccctcagtcacccctcctca 363

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

N_Geneseq_101002.*
1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	313.4	86.3	483	16	AA083491
2	313.4	86.3	483	20	AA083491
3	313.4	86.3	483	20	AA083491
4	311.8	85.9	423	16	AA083492
5	311.8	85.9	423	20	AA083492
6	311.8	85.9	423	20	AA083492
7	303.6	83.6	366	15	AA068709
8	299.2	82.4	738	15	AA070612
9	296.4	81.7	360	17	AA0709300

10	296.4	81.7	417	17	AA0709299
11	291	80.2	418	16	AA075889
12	282	77.7	1413	21	ABR11000
13	269	74.1	354	21	AA514500
14	267	73.6	369	21	AA094646
15	261.8	72.1	429	15	AA064166
16	250.8	69.1	812	14	AA037056
17	250.8	69.1	812	20	AA094079
18	250.8	69.1	812	21	AA051000
19	249.2	68.7	812	21	AA05437
20	195.8	53.9	363	22	AA042390
21	191.4	52.7	423	20	AA045597
22	191.4	52.7	423	20	AA039427
23	191.4	52.7	423	20	AA023965
24	190.6	52.5	423	20	AA079207
25	190.2	52.4	613	16	AA078943
26	185.4	51.1	418	16	AA075916
27	185.4	51.1	1607	22	AA066519
28	184.6	50.9	444	18	AA080181
29	183.8	50.6	418	16	AA075917
30	181.2	49.9	546	16	AA078964
31	181	49.9	437	21	AA042289
32	180.2	49.6	397	22	AA080854
33	179.8	49.5	400	21	AA000033
34	172.6	47.5	630	16	AA078948
35	171	47.1	423	16	AA083493
36	171	47.1	423	20	AA085887
37	171	47.1	423	20	AA079516
38	168.8	46.5	447	20	AA020406
39	168.4	46.4	646	24	ABR39075
40	165	45.5	714	18	AA086310
41	165	45.5	714	24	ABR92027
42	165	45.5	1173	18	AA086312
43	163.2	45.0	378	18	AA061237
44	163.2	45.0	1428	18	AA061279
45	162	44.6	477	20	AA020408

ALIGNMENTS

RESULT 1	AA083491	standard; cDNA; 483 BP.
ID	AA083491	
XX	AA083491	
AC	20-SEP-1995	(first entry)
XX		
DE	Mouse MAB 3B9 heavy chain.	
XX		
KW	Chimeric antibody; humanized antibody; antibody engineering;	
KW	monoclonal antibody; MAB; interleukin-4; IL-4; allergy; ds.	
XX		
OS	Mus sp.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	64..483
FT		/*tag- a
FT	sig-peptide	64..120
FT		/*tag- b
FT	mat-peptide	121..483
FT		/*tag- c
XX		
PN	W09507301-A.	
XX		
PD	16-MAR-1995.	
XX		
PF	07-SEP-1994;	94WO-US10308.
XX		
PR	07-SEP-1993;	93US-0117366.
PR	14-OCT-1993;	93US-0136783.
XX		

Murine anti-Protein heavy chain
DNA encoding prote
Sequence #1 in
Mouse antibody 136
Sequence of mouse
Rat immunoglobulin
KM50 Rat immunoglob
Rat activated immu
KM50 cell-derived
Nucleotide sequenc
Sequence encoding
Antibody B17X2 VH
Human B17X2 antibo
Anti-HIV-1 gp120 a
Human immunoglobul
Anti-human IL-6 ch
Human immune syste
Monoclonal antibod
Anti-human IL-6 ch
Human immunoglobul
Human 5' EST Isola
Human anti-HIV gp1
Human secreted pro
Human immunoglobul
Humanized antibody
Heavy chain variab
Heavy chain coding
IgG antibody 2.4.4
cDNA encoding lung
Single chain anti-
Anti-disialosyl
Single chain anti-
Human anti-RSV mon
Human anti-RSV mon
IgG antibody 2.3.2

PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Gross MS, Holmes SD, Sylvester DR;
 XX
 XX WPI: 1995-123387/16.
 DR P-PSDB; AAR70190.
 XX
 XX Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
 PT from high affinity mabs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 XX
 XX Disclosure; Fig. 2; 97pp; English.
 PS
 XX Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. CDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEMT+ and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (AA083490-91), and used for
 CC antibody engineering.

Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

Query Match 86.3%; Score 313.4; DB 16; Length 483;
 Best Local Similarity 91.5%; Pred. No. 1.8e-86;
 Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCTAGTCTG 60
 DB 121 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCTAGTCTG 180
 OY 61 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTGAGCTGGATTGCA 120
 DB 181 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTGAGCTGGATTGCA 240
 OY 121 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTTACTGGATGATGACAGCCG 180
 DB 241 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTTACTGGATGATGACAGCCG 300
 OY 181 TATTAACCCATCCCTGAAGAGCCGCTTACATCTCCAAAGATATCTCCAGCAACAGGTA 240
 DB 301 TATTAACCCATCCCTGAAGAGCCGCTTACATCTCCAAAGATATCTCCAGCAACAGGTA 360
 OY 241 TTCTCTCAAGATCACCAGTGTGAGACATCGAGATACCTCCACATACACTGCTGCTGAGA 300
 DB 361 TTCTCTCAAGATCACCAGTGTGAGACATCGAGATACCTCCACATACACTGCTGCTGAGA 420
 OY 301 GTCTCTTACTGCTGCTATGCTATGAGACTACTGGGGTCAAGGAACTGATCAGCGTCTCC 360
 DB 421 GAGACTGTGTTTACTGCTGCTATGCTGATGCTGGGGCCAGGAGCACGATCAGCGTCTCC 480
 OY 361 TCA 363
 DB 481 TCA 483

RESULT 2
 AAX85885
 ID AAX85885 standard; CDNA; 483 BP.

AC AAX85885;

DT 13-SEP-1999 (first entry)

XX Heavy chain variable region CDNA of murine IL-4 antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;

KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;

KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;

KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;

KW rheumatoid arthritis; host-versus-graft disease; renal disease;

XX allergy; ds.

OS Mus sp.
 XX
 XX US928904-A.
 XX
 XX 27-JUL-1999.
 XX
 XX
 XX 07-JUN-1995; 95US-0483632.
 XX
 XX 07-JUN-1995; 95US-0483632.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-0510308.
 XX
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Gross MS, Holmes SD, Sylvester DR;
 XX
 XX WPI: 1999-429500/36.
 DR P-PSDB; AAY23768.
 XX
 XX
 PT New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 XX
 XX Claim 3; Fig 2; 50pp; English.

The present sequence encodes the heavy chain variable region of
 CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used
 CC in the production of chimeric and humanised IL-4 monoclonal antibodies.
 CC The antibodies of the invention are used in therapeutic and
 CC pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.

Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

Query Match 86.3%; Score 313.4; DB 20; Length 483;
 Best Local Similarity 91.5%; Pred. No. 1.8e-86;
 Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCTAGTCTG 60
 DB 121 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCTAGTCTG 180
 OY 61 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTGAGCTGGATTGCA 120
 DB 181 ACTTGTCTTCTCTCTGCTGCTTTCACAGCACTTCTGTATGGGTGTGAGCTGGATTGCA 240
 OY 121 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTTACTGGATGATGACAGCCG 180
 DB 241 CAGGCTTCAGGAAGGCTCTGAGTGGCTGGCAGACATTTTACTGGATGATGACAGCCG 300
 OY 181 TATTAACCCATCCCTGAAGAGCCGCTTACATCTCCAAAGATATCTCCAGCAACAGGTA 240
 DB 301 TATTAACCCATCCCTGAAGAGCCGCTTACATCTCCAAAGATATCTCCAGCAACAGGTA 360
 OY 241 TTCTCTCAAGATCACCAGTGTGAGACATCGAGATACCTCCACATACACTGCTGCTGAGA 300
 DB 361 TTCTCTCAAGATCACCAGTGTGAGACATCGAGATACCTCCACATACACTGCTGCTGAGA 420
 OY 301 GTCTCTTACTGCTGCTATGCTATGAGACTACTGGGGTCAAGGAACTGATCAGCGTCTCC 360
 DB 421 GAGACTGTGTTTACTGCTGCTATGCTGATGCTGGGGCCAGGAGCACGATCAGCGTCTCC 480
 OY 361 TCA 363
 DB 481 TCA 483

XX	AAAX79520 standard; cDNA; 483 BP.
XX	AAAX79520;
AC	11-AUG-1999 (first entry)
DT	
XX	Heavy chain coding sequence for murine 3B9 antibody.
DE	
XX	Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
KW	allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
KV	atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
KX	autoimmune disease; graft versus host disease; ss.
XX	
OS	Mus sp.
XX	
PN	US5914110-A.
XX	22-JUN-1999.
PF	07-JUN-1995; 95US-0483636.
XX	
PR	07-JUN-1995; 95US-0483636.
PR	07-SEP-1993; 93US-0113766.
PR	14-OCT-1993; 93US-0136783.
PR	07-SEP-1994; 94WO-0510308.
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
XX	
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 1999-370482/31.
DR	P-PsDB; AAY18121.
XX	
PT	Recombinant IL4 antibodies
XX	
XX	Disclosure; Fig 2; 50pp; English.
CC	This sequence encodes the heavy chain of the murine 3B9
CC	antibody of the invention. The antibody is a chimeric or
CC	humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
CC	immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
CC	the treatment of allergic disorders such as allergic rhinitis,
CC	conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
CC	The antibodies are also useful for regulating B and T cell proliferation
CC	and as such are useful in the treatment of autoimmune diseases and graft
CC	versus host disease.
XX	
SQ	Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;
XX	
Query Match	86.3%; Score 313.4; DB 20; Length 483;
Best Local Similarity	91.5%; Pred. No. 1,8e-86;
Matches 332; Conservative	0; Mismatches 31; Indels 0; Gaps 0;
OY	I CAGGTACTCTGGAAGAGCTGGCGCCCTGGATATTGCAGCCCTCCAGACCCTCAGTCTG 60
Db	121 CAGGTACTCTGGAAGAGCTGGCGCCCTGGATATTGCAGCCCTCCAGACCCTCAGTCTG 180
OY	61 ACTTGTTCTTCTCTGCGGTTTTCACTGAGCACCTTGGTAGGCGTGTGAGCTGATTCGA 120
Db	181 ACTTGTTCTTCTCTGCGGTTTTCACTGAGCACCTTGGTAGGCGTGTGAGCTGATTCGT 240
OY	121 CAGCCTTCAGGAAAAGGCTGTGAGTGGCTGGCGACACATTTACTGGATGATGACAAGGCC 180
Db	241 CAGCCTTCAGGAAAAGGCTGTGAGTGGCTGGCGACACATTTACTGGATGATGACAAGGCC 300
OY	181 TATAAACCATCCCTGAGAAGCGCGCTTCAATCTCCAAGAGATACTCCAGAACCAAGTA 240
Db	301 TATAAACCATCCCTGAGAAGCGCGCTCAATCTCCAAGAGATACTCCAGAACCAAGTA 360
OY	241 TTCTCATGATACCAAGTGTGTGACACTGAGATACTGCCACATACTACTGTCTGGAAG 300

DB	361	TTCCCAAGATACACAGTGTGACACTGACAGATACCTGACATACACTGTGTGTCAGAA	420
OY	301	GTCTTCTACATGCTATGCTATGGACTACTAGGAGGTCAGAGAACCTCAGTCAACGTCCTC	360
DB	421	GAGACTGTGTCTACTGGTACTTCGATGTCTGGGGCGACAGGACACAGGTCACCGTCCTC	480
OY	361	TCA 363	
DB	481	TCA 483	
RESULT 4			
AA083492	ID	AA083492 standard; cDNA; 423 BP.	
XX	AC	AA083492;	
XX	DT	20-SEP-1995 (first entry)	
XX	DE	Chimeric antibody 3B9 heavy chain.	
XX	DE	Chimeric antibody; antibody engineering; monoclonal antibody;	
KW	KW	MAb; interleukin-4; IL-4; allergy; ds.	
XX	OS	Homo sapiens; Mus sp.	
XX	Key	Location/Qualifiers	
FF	CDS	1..423	
FT		/*tag= a	
FT		1..57	
FT		/*tag= b	
FT		58..423	
FT		/*tag= c	
XX	PN	W09507301-A.	
XX	PD	16-MAR-1995.	
XX	PF	07-SEP-1994; 94MO-US10308.	
XX	PR	07-SEP-1993; 93US-0117366.	
XX	PR	14-OCT-1993; 93US-0136783.	
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX	PA	(SMIK) SMITHKLINE BEECHAM PLC.	
XX	PI	Gross MS, Holmes SD, Sylvester DR;	
XX	DR	WPI; 1995-123387/16.	
XX	DR	P-PSDB; AAR70191.	
XX	PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived	
XX	PT	from high affinity mAbs - useful in treatment of IL-4-mediated	
XX	PT	and IgE-mediated allergic conditions	
XX	PS	Disclosure; Fig.3; 97pp; English.	
XX	CC	A human/mouse chimeric antibody heavy chain variable region was	
XX	CC	constructed (given in AAR70191) that contained the mouse anti-human	
XX	CC	IL-4 MAb 3B9 variable region including 3 CDSs (AAR70196-200) and a	
XX	CC	human antibody signal peptide (AAR70193). The construct was used	
XX	CC	for humanized antibody production.	
XX	CC	Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;	
OY	Query Match	85.9%; Score 311.8; DB 16; Length 423;	
OY	Best Local Similarity	91.2%; Pred. No. 5..4e-86;	
OY	Matches 331; Conservative	0; Mismatches 32; Indels 0; Gaps 0	
DB	1	CAGGTACTCTGGAAGAGCTGCGCCCTGGGATATGACACCCCTCCAGACCCCTCACTCTG	60
DB	61	CAGGTACTCTGGAAGAGCTGCGCCCTGGGATATGACACCCCTCCAGACCCCTCACTCTG	120

QY 61 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTCGA 120
 Db 121 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTCGT 180
 QY 121 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCC 180
 Db 181 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCC 240
 QY 181 TATACCCATCCCTGAGAGCCGCTTACAAATCTCCAGAGTACTCTCAGAACAGGTA 240
 Db 241 TATACCCATCCCTGAGAGCCGCTTACAAATCTCCAGAGTACTCTCAGAACAGGTA 300
 QY 241 TTCCTCAAGATCACCAGTGTGACACATCGAGATCTGCCAATCTACTGTCTCGAAG 300
 Db 301 TTCCTCAAGATCACCAGTGTGACACATCGAGATCTGCCAATCTACTGTCTCGAAG 360
 QY 301 GTCTCTTAAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 360
 Db 361 GAGACTGTGTCTACTGTGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 421 TCA 423
 Db 421 TCA 423
 RESULT 5
 AAX85886
 ID AAX85886 standard; cDNA; 423 BP.
 AC AAX85886:
 DT 13-SEP-1999 (first entry)
 XX
 DE Heavy chain variable region cDNA of murine/human chimeric antibody 3B9.
 XX
 KW Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy; ds.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN US928904-A.
 XX
 XX 27-JUL-1999.
 XX
 XX 07-JUN-1995; 95US-0483632.
 PR 07-JUN-1995; 95US-0483632.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 DR WPI: 1999-429500/36.
 DR P-PSDB: AAY23769.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 XX
 XX Example 3; Fig 3; 50pp; English.
 PS The present sequence encodes the heavy chain variable region of
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
 CC specification describes chimeric and humanised IL-4 monoclonal
 CC

CC antibodies. The antibodies of the invention are used in therapeutic
 CC and pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 XX
 SO Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;
 Query Match 85.9%; Score 311.8; DB 20; Length 423;
 Best Local Similarity 91.2%; Pred. No. 5.4e-86;
 Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 1 CAGGTTACTCTGAGAAAGTCTGGGCTGGGATATGAGCCCTCCAGACCCTCAGTCTG 60
 Db 61 CAGGTTACTCTGAGAAAGTCTGGGCTGGGATATGAGCCCTCCAGACCCTCAGTCTG 120
 QY 61 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTCGA 120
 Db 121 ACTGTTCTTCTCTGCGTTTTCACAGACATTCGTATGGGTGAGCTGATTCGT 180
 QY 121 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCC 180
 Db 181 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCC 240
 QY 181 TATACCCATCCCTGAGAGCCGCTTACAAATCTCCAGAGTACTCTCAGAACAGGTA 240
 Db 241 TATACCCATCCCTGAGAGCCGCTTACAAATCTCCAGAGTACTCTCAGAACAGGTA 300
 QY 241 TTCCTCAAGATCACCAGTGTGACACATCGAGATCTGCCAATCTACTGTCTCGAAG 300
 Db 301 TTCCTCAAGATCACCAGTGTGACACATCGAGATCTGCCAATCTACTGTCTCGAAG 360
 QY 301 GTCTCTTAAGTGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 360
 Db 361 GAGACTGTGTCTACTGTGATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 361 TCA 363
 Db 421 TCA 423
 RESULT 6
 AAX79542
 ID AAX79542 standard; cDNA; 423 BP.
 AC AAX79542:
 DT 11-AUG-1999 (first entry)
 XX
 DE Chimeric 3B9 monoclonal antibody heavy chain coding sequence.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease; ss.
 XX
 OS Synthetic.
 XX
 PN US5914110-A.
 XX
 PD 22-JUN-1999.
 XX
 PE 07-JUN-1995; 95US-0483636.
 PR 07-JUN-1995; 95US-0483636.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI: 1999-370482/31.

DR P-PSDB: AAY18125.

XX Recombinant IL4 antibodies

XX Example 5; Fig 3; 50pp; English.

CC This sequence represents the DNA encoding the light chain of the
CC chimeric 3B9 antibody of the invention. The antibody is a chimeric or
CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
CC the treatment of allergic disorders such as allergic rhinitis,
CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
CC The antibodies are also useful for regulating B and T cell proliferation
CC and as such are useful in the treatment of autoimmune diseases and graft
CC versus host disease.

SO Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;

Query Match 85.9%; Score 311.8; DB 20; Length 423;
Best Local Similarity 91.2%; Pred. No. 5.4e-86;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```

OY 1 CAGGTACTCTGGAAGAAGTCTGCGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 60
   |||||||
DB 61 CAGGTACCCCTGGAAGAAGTCTGCGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 120
OY 61 ACTGTCTCTCTCTGCGGTTTTCACAGCACTTCTGGTATGGGTGAGCTGGATTGCA 120
   |||||||
DB 121 ACTGTCTCTCTCTGCGGTTTTCACAGCACTTCTGGTATGGGTGAGCTGGATTGCT 180
OY 121 CAGCCTTCAGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 180
   |||||||
DB 181 CAGCCTTCAGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 240
OY 181 TATAACCCATCCCTGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 240
   |||||||
DB 241 TATAACCCATCCCTGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 300
OY 241 TTCCTCAAGATCACCAGTGTGAGACATCTGAGATAGTGCACATCTACTGCTGCAAGG 300
   |||||||
DB 301 TTCCTCAAGATCACCAGTGTGAGACATCTGAGATAGTGCACATCTACTGCTGCTGCAAGA 360
   |||||||
DB 301 GTCTCTTACTGCTTATGATGATGACTACTGCGGTCAGGAACCTCAGTCCGCTCC 360
   |||||||
DB 361 GAGACTGTGTCTACTGCTGATGATGCTGCGGCGCAGGACACGCTCAGCTCC 420
OY 361 TCA 363
   |||
DB 421 TCA 423

```

RESULT 7

AA068709 standard; cDNA to mRNA; 366 BP.

XX AA068709;

XX 08-FEB-1995 (first entry)

XX Humanised Mab H-chain coding sequence.

XX Human; mouse; murine; heavy; light; chain; monoclonal; antibody;

XX complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN; ds.

OS Chimeric - Mus musculus.

XX Chimeric - Homo sapiens.

XX JP06141885-A.

XX 24-MAY-1994.

XX 05-NOV-1992; 92JP-0322476.

XX 05-NOV-1992; 92JP-0322476.

XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKUYUSHO.

XX WPI: 1994-205040/25.

DR P-PSDB: AAR54101.

XX Recombinant anti-HIV monoclonal antibody - capable of

XX neutralising strains which can not be neutralised by anti-IIIB

XX and IIIMN antibodies

XX Disclosure; Page 13; 23pp; Japanese.

CC The sequences given in AA068709-10 encode the heavy and light chains
CC respectively of the humanised monoclonal antibody (Mab) of the
CC invention. The antibody has the ability to neutralise human
CC immunodeficiency virus. The antibody is classified as IgG kappa and
CC has the sequence RIGPR or RVGPR in the principal neutralising
CC domain. The antibody may be used to neutralise the clinically
CC separate strains which cannot be neutralised by the neutralising
CC antibodies against IIIB and IIIMN strains.

SO Sequence 366 BP; 85 A; 98 C; 84 G; 99 T; 0 other;

Query Match 83.6%; Score 303.6; DB 15; Length 366;
Best Local Similarity 91.3%; Pred. No. 1.7e-83;
Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

```

OY 1 CAGGTACTCTGGAAGAAGTCTGCGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 60
   |||||||
DB 1 CAGGTACTCTGGAAGAAGTCTGCGCCCTGGGATATTGACAGCCCTCCAGACCTCACTCTG 60
OY 61 ACTGTCTCTCTCTGCGGTTTTCACAGCACTTCTGGTATGGGTGAGCTGGATTGCA 120
   |||||||
DB 61 ACTGTCTCTCTCTGCGGTTTTCACAGCACTTCTGGTATGGGTGAGCTGGATTGCT 120
OY 121 CAGCCTTCAGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 180
   |||||||
DB 121 CAGCCTTCAGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 180
OY 121 TTCCTCAAGATCACCAGTGTGAGACATCTGAGATAGTGCACATCTACTGCTGCAAGG 300
   |||||||
DB 181 TATAACCCATCCCTGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 240
   |||||||
DB 181 TATAACCCATCCCTGGAAGAAGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAAGCGC 300
OY 241 TTCCTCAAGATCACCAGTGTGAGACATCTGAGATAGTGCACATCTACTGCTGCTGCAAGG 300
   |||||||
DB 241 TTCCTCAAGATCACCAGTGTGAGACATCTGAGATAGTGCACATCTACTGCTGCTGCAAGG 300
   |||||||
DB 241 GTCTCTTACTGCTTATGATGATGACTACTGCGGTCAGGAACCTCAGTCCGCTCC 357
   |||||||
DB 301 GTCTCTTACTGCTTATGATGATGACTACTGCGGTCAGGAACCTCAGTCCGCTCC 360
OY 358 TCCTCA 363
   |||||
DB 361 TCCTCA 366

```

RESULT 8

AA070612 standard; DNA; 738 BP.

XX AA070612;

XX 28-APR-1995 (first entry)

XX IL-6 binding inhibitor DNA.

XX Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;

KW septic shock; multiple myeloma; ss.
 XX Homo sapiens.
 XX EPI17126-A.
 XX 28-SEP-1994.
 XX 16-FEB-1994; 94EP-0102346.
 XX 17-FEB-1993; 93JP-0028173.
 XX (AJIN) AJINOMOTO KK.
 XX Hamuro J, Nakazawa H, Shimamura T;
 XX WPI: 1994-295777/37.
 XX P-PSDB: AAR58612.
 DR Polypeptide inhibiting binding of human interleukin-6 (IL-6) to
 PT its receptor - useful for treating auto-immune disease induced
 PS or aggravated by IL-6
 PS Claim 9; Page 19; 26pp: English.
 CC AAG70612 codes for human interleukin-6 binding inhibitor, the
 CC polypeptide described in AAR58612. This polypeptide inhibits the
 CC binding of human IL-6 to its receptor, and can therefore be
 CC useful in the treatment of a variety of autoimmune diseases;
 CC specifically in the treatment of rheumatoid arthritis, septic
 CC shock due to bacterial infection and multiple myeloma.
 XX
 SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T; 0 other;
 Query Match 82.4%; Score 299.2; DB 15; Length 738;
 Best Local Similarity 90.1%; Pred. No. 4.9e-82;
 Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;
 QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 60
 DB 367 CAGGTCAAACTCGAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 426
 QY 61 ACTTGTCTTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGATTCGA 120
 DB 427 ACTTGTCTTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGATTCGT 486
 QY 121 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 180
 DB 487 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 546
 DB 181 TATTAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
 DB 547 TATTAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 606
 QY 241 TTCTCTAAGATCAACATGTGGACATCGAGATCTCCACATCTACTGTGCTCGAAG- 299
 DB 607 TTCTCTAAGATCAACATGTGGACATCGAGATCTCCACATCTACTGTGCTCGAAG- 666
 QY 300 -----GGTCTCTTAAGCTATGCTATGAGTACTGAGGAGTCAAGAACTCAGTC 351
 DB 667 AGTCTATATGTAATTTGGGGGAGCTATGATGAGTACTGAGGAGTCAAGAACTCAGTC 726
 QY 352 ACCGTCCTCA 363
 DB 727 ACCGTCCTCA 738
 RESULT 9
 ID AAT09300 standard; DNA: 360 BP.
 XX
 AC AAT09300;
 XX

DT 25-JUL-1996 (first entry)
 XX
 DE Murine anti-Protein C MAb HPC-4 VH gamma mature protein coding region.
 XX
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 KW zymogen; cleavage; mouse; humanised antibody; variable region;
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.
 XX
 OS Mus musculus.
 XX
 PN W09534652-A1.
 XX
 PD 21-DEC-1995.
 XX
 PE 09-JUN-1995; 95WO-US07372.
 XX
 PR 10-JUN-1994; 94US-0259321.
 XX
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 XX
 PI Esmon CT, Rezaie A;
 XX
 DR WPI: 1996-049681/05.
 DR P-PSDB: AAR8109.
 XX
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -
 PT inhibits Protein C anticoagulant activation by
 PT thrombin-thrombomodulin, e.g. for treating tumours
 PS
 PS Claim 4; Page 30; 41pp: English.
 XX
 CC This is the nucleotide sequence encoding the mature protein from the
 CC murine anti-protein C monoclonal antibody HPC-4 heavy chain variable
 CC region (VH gamma). HPC-4 recognises the activation peptide region
 CC (AAR8106) of the heavy chain of protein C, a vitamin K-dependent plasma
 CC protein zymogen. Protein C is activated to activated protein C (APC)
 CC by cleavage between the Arg-Leu amino acid contained within the
 CC activation peptide sequence. HPC-4 prevents protein C activation to
 CC APC by binding to this region. The DNA sequences encoding the variable
 CC regions of the heavy and light chains of the antibody (AAT09299-302)
 CC were used to construct humanised antibodies using the PCR primers
 CC AAT09303-9. The humanised antibodies are useful as inhibitors of
 CC coagulation and can be used for the treatment of tumours by inhibiting
 CC the anticoagulant activity of APC by preventing conversion of protein C
 CC to APC.
 XX
 SQ Sequence 360 BP; 82 A; 91 C; 95 G; 92 T; 0 other;
 Query Match 81.7%; Score 296.4; DB 17; Length 360;
 Best Local Similarity 90.6%; Pred. No. 2.8e-81;
 Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
 QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 60
 DB 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 60
 QY 61 ACTTGTCTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGATTCGA 120
 DB 61 ACTTGTCTCTCTCTGGGTTTTCACAGCACTTCTGTATGGGTGAGCTGATTCGT 120
 QY 121 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 180
 DB 121 CAGCCTTCAGAAAGAGTCTGGAGTGGTGGCAGACATTTACTGGATGACAAAGCG 180
 QY 181 TATTAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
 DB 181 TATTAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
 QY 241 TTCTCTAAGATCAACATGTGGACATCGAGATCTCCACATCTACTGTGCTCGAAG 300
 DB 241 TTCTCTAAGATCAACATGTGGACATCGAGATCTCCACATCTACTGTGCTCGAAG 300
 QY 301 GTCTCTTAAGTCTATGCTATGAGTACTGGGGTCAAGAACTCAGTCAACGCTCTCC 360

.....

PS Claim 10; Page 49; 82pp; Japanese
 YY

CC The sequence of the gene encoding the heavy chain variable region of
 CC the mouse anti-human Interleukin-6 (IL-6) antibody. The fragment was
 CC amplified by primers (AA075876-87) from cDNA derived from mRNA from
 CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19
 CC to produce plasmid pUC-SK2-Vh. The inserted fragment is used to
 CC generate constructs (see AA075914-7) encoding fragments of an antibody to
 CC the human IL-6 comprising (a) a light chain with (1) a variable region
 CC containing 3 complementarily determining regions (CDR) (AA07201-3)
 CC inserted into several framework regions (FR) (AA07204-7) and (11) a human
 CC light chain constant region and (b) a heavy chain with (1) a variable
 CC region containing 3 CDR (AA07212-4) inserted into an FR (AA07215-8) and
 CC (11) a human light chain constant region. The FR of the light chain may
 CC be mouse derived (AA075888) or from the human antibody REI. The heavy
 CC chain FR may also be mouse derived (AA075889) or from the human antibody
 CC DMW. The antibodies can be used in the treatment of IL-6 related
 CC disorders. The antibodies are useful as they have low antigenicity due to
 CC the use of human derived sequences and low antigenicity mouse derived
 CC sequences.

XX Sequence 418 BP; 96 A; 113 C; 99 G; 110 T; 0 other;

SO Query Match

Best Local Similarity 80.2%; Score 291; DB 16; Length 418;

Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 CAGGTTACTGTGAAAGAGTGTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
 DB 58 CAGGTTACTGTGAAAGAGTGTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 117
 QY 61 ACTTGTCTTCTCTGCTGCTTTCACAGCACTTCTGATAGGTGAGCTGATTCGA 120
 DB 118 ACTTGTCTTCTCTGCTGCTTTCACAGCACTTCTGATAGGTGAGCTGATTCGT 177
 QY 121 CAGCCTTCAGAAAGAGTGTGAGTGGCTGGACACATTTACTGGATGATGACACGCC 180
 DB 178 CAGCCTTCAGAAAGAGTGTGAGTGGCTGGACACATTTACTGGATGATGATGATGAC 237
 QY 181 TATTAACCATCCCTGAAAGAGCGGCTTACAACTCCAGATACCTCCAGCAACAGTA 240
 DB 238 TATTAACCATCCCTGAAAGAGCGGCTTACAACTCCAGATACCTCCAGCAACAGTA 297
 QY 241 TTCTCTCAAGATCCAGTGTGACATCGAGATCTCCCATCTACTGCTGCGAAGG 300
 DB 298 TTCTCTCAAGATCCAGTGTGACATCGAGATCTCCCATCTACTGCTGCGAATG 357
 QY 301 GTCCTCTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 DB 358 GAGGAT---TACGACGAAGCTATGAGTACTGAGGCTCAAGGAACCTCAGTCACCGTCTCC 414
 361 TCA 363
 415 TCA 417

RESULT 12

ID ABK11000 standard; DNA; 1413 BP.

AC ABK11000;

DT 06-JUN-2002 (first entry)

DE DNA encoding protein #2 in invention relating to von Willebrand factor.

KM Von Willebrand factor; gene; ds.

OS Unidentified.

XX Key Location/Qualifiers

FT CDS 1..1413

FT /*tag- a

XX /product- "Protein #2"

PN KR99066382-A.
 XX 16-AUG-1999.
 PD 24-JAN-1998; 98KR-0002265.
 XX 24-JAN-1998; 98KR-0002265.
 PR 24-JAN-1998; 98KR-0002265.
 XX (GRC) KOREA GREEN CROSS CORP.
 PA
 PI Kim HC, Kim JS, Byun TH, Lee JS, Oh HG, Lee JM, Kim BJ;
 DR WPL: 2000-547436/50.
 DR P-PSDB: AAU77289.
 XX Method for purifying factor VIII using chimera antibody to von
 PT Willebrand factor -
 PS Disclosure; Fig 2; 12pp; Korean.
 CC The present invention relates to von Willebrand factor. The present
 CC sequence encoding a protein of unknown function is given in the
 CC specification of the present invention.

SO Sequence 1413 BP; 326 A; 445 C; 373 G; 269 T; 0 other;

Query Match

Best Local Similarity 77.7%; Score 282; DB 21; Length 1413;

Matches 312; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 2 AGGTTACTGTGAAAGAGTGTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTGA 61
 DB 59 AAGTGAAGCTGAGAGAGTGTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTGA 118
 QY 62 CTGCTCTCTCTGCTGCTTTCACAGCACTTCTGATAGGTGAGCTGATTCGAC 121
 DB 119 CTGCTCTCTCTGCTGCTTTCACAGCACTTCTGATAGGTGAGCTGATTCGTC 178
 QY 122 AGCCTTCAGAAAGAGTGTGAGTGGCTGGACACATTTACTGGATGATGACACGCC 181
 DB 179 AGCCTTCAGAAAGAGTGTGAGTGGCTGGACACATTTACTGGATGATGATGATGAC 238
 QY 182 ATTAACCATCCCTGAAAGAGCGGCTTACAACTCCAGATACCTCCAGCAACAGTA 241
 DB 239 ATTAACCATCCCTGAAAGAGCGGCTTACAACTCCAGATACCTCCAGCAACAGTA 298
 QY 242 TTCTCTCAAGATCCAGTGTGACATCGAGATCTCCCATCTACTGCTGCGAAGG 301
 DB 299 TTCTCTCAAGATCCAGTGTGACATCGAGATCTCCCATCTACTGCTGCGAATG 358
 QY 302 TCTCTCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 361
 DB 359 GAAACAGGAGGAGGAGTGTGCTTGTCTTACTGAGGCTCAAGGAACCTCAGTCACCGTCTCT 418
 362 CA 363
 419 CA 420

RESULT 13

ID AAS14500 standard; DNA; 354 BP.

AC AAS14500;

DT 06-JUN-2002 (first entry)

DE DNA sequence #1 in invention relating to von Willebrand factor.

KM Von Willebrand factor; ds.

OS Unidentified.

PN KR9066382-A.
 XX 16-AUG-1999.
 XX 24-JAN-1998; 98KR-0002265.
 XX 24-JAN-1998; 98KR-0002265.
 XX (GRC) KOREA GREEN CROSS CORP.
 PA Kim HC, Kim JS, Byun TH, Lee JS, Oh HG, Lee JM, Kim BJ;
 DR WPI: 2000-547436/50.
 XX Method for purifying factor VIII using chimera antibody to von
 PT Willebrand factor -
 XX Claim 5; Page 7; 12pp; Korean.
 The present invention relates to von Willebrand factor. The present
 CC DNA sequence of unknown function is given in the specification of
 the present invention.
 XX Sequence 354 BP; 76 A; 97 C; 98 G; 83 T; 0 other;

Query Match 74.1%; Score 269; DB 21; Length 354;
 Best Local Similarity 86.6%; Pred. No. 7.4e-73;
 Matches 309; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 60
 DB 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 60
 QY 61 ACTTGTCTTCTCTCTGGGTTTCTACAGACCTTCTGGTATGGGTGAGCTGAGTTGCA 120
 DB 61 ACTTGTCTTCTCTCTGGGTTTCTACAGACCTTCTGGTATGGGTGAGCTGAGTTGCGT 120
 QY 121 CAGCCTTCAGGAAGGCTGTGGATGGCTGGCAGACATTTACTGGGATGTGCAAGCCG 180
 DB 121 CAGCCTTCAGGAAGGCTGTGGATGGCTGGCAGACATTTACTGGGATGTGCAAGCCG 177
 QY 181 TATATCCCATCCCTGAAGACCGGCTTACATCTCCAAAGATACCTCCAGCAACAGGTA 240
 DB 178 TATATCCCATCCCTGAAGACCGGCTTACATCTCCAAAGATACCTCCAGCAACAGGTA 237
 QY 241 TTCTCTCAAGTCAACAGTGTGGACACTCGAGATACCTCCATACCTACTGCTCGAAG 300
 DB 238 TTCTCTCAAGTCAACAGTGTGGACACTCGAGATACCTCCATACCTACTGCTCGAAG 297
 QY 301 GTCTCTCTAATCTGCTATGCTATGAGTCTGGGGTCAAGAACCTCAGTACCGTC 357
 DB 298 GGAACAAGGAGCGGACCTGTTGCTTACTGGGGCCAAAGAACCTCAGTACCGTC 354

RESULT 14
 ID AAA99646 standard; cDNA; 369 BP.
 XX AAA99646;
 AC
 XX 25-JAN-2001 (first entry)
 DE Mouse antibody 1369 heavy chain variable region cDNA.
 XX
 XX Mouse: antibody 1369; antitumor; immunosuppressive; neuroprotective;
 KW anti-inflammatory; antiproliferative; interleukin-18; IL-18;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KM type I diabetes; insulin dependent diabetes; IDDM; psoriasis;
 KM inflammatory bowel disease; complementarity determining region; CDR; ss.
 XX Mus musculus.
 OS
 XX
 FH Key Location/Qualifiers

FT CDS 1..369
 FT /tag- a
 FT /partial
 FT /product= "antibody 1369 heavy chain variable region"
 PN WO200056771-A1.
 XX 28-SEP-2000.
 XX 17-MAR-2000; 2000WO-US07349.
 XX 19-MAR-1999; 99US-0125299.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Ho YS, Holmes SD, Taylor AH, Abdel-Meguid SS;
 DR WPI: 2000-628249/60.
 DR P-PDB; AAB21367.

Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal
 PT antibody having high affinity and useful for treating IL-18 mediated
 PT disorders such as multiple sclerosis, rheumatoid arthritis and
 PT psoriasis -
 XX Claim 4; Fig 4; 64pp; English.

The present sequence encodes the heavy chain variable region of the mouse
 CC antibody 1369. The antibody has high affinity for human interleukin-18
 CC (IL-18) and is useful for treating and diagnosing IL-18-mediated
 CC disorders, e.g. autoimmune diseases such as multiple sclerosis,
 CC rheumatoid arthritis, type I or insulin dependent diabetes, inflammatory
 CC bowel disease and psoriasis. Specific changes can be introduced
 CC into the nucleotide sequences encoding the complementarity determining
 CC regions (CDRs) or framework regions of the variable light chain and
 CC heavy chain peptides. The resulting modified or fusion nucleic acid
 CC sequences can then be introduced into a plasmid for expression.

Sequence 369 BP; 81 A; 96 C; 89 G; 103 T; 0 other;

Query Match 73.6%; Score 267; DB 21; Length 369;
 Best Local Similarity 84.8%; Pred. No. 3.1e-72;
 Matches 313; Conservative 0; Mismatches 50; Indels 6; Gaps 1;

QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 60
 DB 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 60
 QY 61 ACTTGTCTTCTCTCTGGGTTTCTACAGACCTTCTGGTATGGGTGAGCTGAGTTGCA 120
 DB 61 ACTTGTCTTCTCTCTGGGTTTCTACAGACCTTCTGGTATGGGTGAGCTGAGTTGCGT 120
 QY 121 CAGCCTTCAGGAAGGCTGTGGATGGCTGGCAGACATTTACTGGGATGTGCAAGCCG 180
 DB 121 CAGCCTTCAGGAAGGCTGTGGATGGCTGGCAGACATTTACTGGGATGTATTAAGTAT 180
 QY 181 TATATCCCATCCCTGAAGACCGGCTTACATCTCCAAAGATACCTCCAGCAACAGGTA 240
 DB 181 TATATCCCATCCCTGAAGACCGGCTTACATCTCCAAAGATACCTCCAGCAACAGGTA 240
 QY 241 TTCTCTCAAGTCAACAGTGTGGACACTCGAGATACCTCCATACCTACTGCTCGAAG 300
 DB 241 TTCTCTCAAGTCAACAGTGTGGACACTCGAGATACCTCCATACCTACTGCTCGAAT 300
 QY 297 --AAGGTCCTCTTACTGCTATGCTATGAGTCTGGGGTCAAGAACCTCAGTACCC 354
 DB 301 CATTAGAGCGGTGTAGCTCTCGCTATGAGTCTAGGAGTCAAGAACCTCAGTACCC 360
 QY 355 GTCTCTCTCA 363
 DB 361 GTCTCTCTCA 369

RESULT 15

AA064166 standard; cDNA to mRNA; 429 BP.

AA064166;

29-DEC-1994 (first entry)

Sequence of mouse VH showing the sequences of recombinant anti-FHV-1 antibody CDRs 1, 2 and 3.

Feline herpes virus; FHV-1; monoclonal antibody; CDR; complementarity determining region; ss.

Mus musculus.

Key Location/Qualifiers

1..429

misc_feature

/*tag= a

19

misc_feature

/*tag= b

/label= MHL341

misc_feature

/*tag= c

/label= MCH3

MO9412661-A.

09-JUN-1994.

25-NOV-1993; 93WO-JP01724.

28-NOV-1992; 92JP-0341255.

(KAGA) CHEMO SERO THERAPEUTIC RES INST.

Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;

WPI: 1994-200288/24.

P-PSDB; AAR54092.

Feline monoclonal antibody and recombinant antibodies specific for FHV-1 - for detection, treatment and prevention of FHV-1 infection.

Disclosure; Page 17-18; 53pp; Japanese.

The inventors claim a monoclonal antibody against feline herpes virus (FHV-1). They also claim a recombinant antibody against FHV-1 and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are used in the detection, treatment and prevention of FHV-1. The sequences of the CDRs in the VH of the recombinant anti-FHV-1 antibody are given in AAR54092. The sequences of the CDRs in the VL of the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR sequences are claimed.

Sequence 429 BP; 84 A; 116 C; 109 G; 120 T; 0 other;

Query Match 72.1%; Score 261.8; DB 15; Length 429;

Best Local Similarity 92.6%; Pred. No. 1.3e-70; Mismatches 22; Indels 0; Gaps 0;

Matches 275; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 60

58 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCAGTCTG 117

61 ACTGTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

118 ACTGTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 177

121 CAGCCTCAGGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Db 178 CAGCCTCAGGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237

QY 181 TATACCCATCCCTGAAGAGCCGCTTACATCTCCAAAGATATCTCCAGACCAAGGTA 240

Db 238 TATACCCAGCCCTGAAGAGCCGCTTACATCTCCAAAGATATCTCCAGACCAAGGTA 297

QY 241 TTCCCTCAAGATCAGAGTGTGACACTGAGATACCTGACATACCTGCTGCTGCTG 297

Db 298 TTCCCTCAAGATCAGAGTGTGACACTGAGATACCTGACATACCTGCTGCTGCTG 354

Search completed: July 11, 2003, 15:23:58
Job time : 243 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 22:13:44 ; Search time 1856 Seconds

5691.982 Million cell updates/sec

Title: US-09-759-112A-5

Sequence: 1 caggttactctgaaagatc.....cctcagtcacgcgtctctca 363

Scoring table: IDENTITY_NUC

arched: 2054640 seqs, 14551402878 residues

total number of hits satisfying chosen parameters: 4109280

Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	08
1000	1000	1000

Listing first 45 summaries

Database :

2: 'gb_hcg: '

4: gb_om: *

6: gb_pat:1

gb_p1: *

10: gb-ro:1

12: gbs_sy:1
13: gbs_sy:114: ggb_v1:1
15: ggb_v1:116: em_fun
17: em_fun18: em_in:1
19: em_out:1

20: em_om: 1

22: em_ov: 1

24: em_ph: 1

26: em_ro:1

28: em_un: 1

30: em_htg_

32: em_htg_

34: em_htg_

36: em_htg_
37: em_htg_

```
38: em_sy:
39: em_htr
```

40: em_htgc
41: em_htgc

is the number

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	316.6	87.2	360	10	MMHCVR3	X75097 M. musculus
2	314.6	86.7	420	10	AV090903	AV090903 Mus muscu
3	311.8	85.9	426	6	AX458152	AX458152 Sequence
4	305.4	84.1	360	10	MMU22977	U22977 Mus musculus
5	305.4	84.1	360	10	MMU22979	U22979 Mus musculus
6	305.4	84.1	360	10	MMU22994	U22994 Mus musculus
7	303.8	83.7	360	10	MMU22992	U22992 Mus musculus
8	303.6	83.6	366	6	E07584	E07584 Gene Trame
9	300.6	82.8	360	10	MMU22981	U22981 Mus musculus
10	300.6	82.8	360	10	MMU23010	U23010 Mus musculus
11	300.6	82.8	360	10	MMU23013	U23013 Mus musculus
12	300.6	82.8	361	10	MMU23004	U23004 Mus musculus
13	299.6	82.5	360	10	MMU22999	U22999 Mus musculus
14	299.2	82.4	738	6	E07990	E07990 DNA encodin
15	299.2	82.4	738	6	I45910	I45910 Sequence 6
16	298.6	82.3	358	10	MMU23002	U23002 Mus musculus
17	295.8	81.5	360	10	MMU22983	U22983 Mus musculus
18	295.8	81.5	360	10	MMU22984	U22984 Mus musculus
19	295.8	81.5	360	10	MMU23005	U23005 Mus musculus
20	295.8	81.5	360	10	MMU23009	U23009 Mus musculus
21	294.4	81.1	360	10	MMU22997	U22997 Mus musculus
22	294.2	81.0	366	10	MM1G5MT	X53097 Mouse mRNA
23	293.8	80.9	358	10	MMU23000	U23000 Mus musculus
24	293.4	80.8	359	10	MMU23007	U23007 Mus musculus
25	293.2	80.8	438	10	S75897	S75897 Ig VH-IgG h
26	291.4	80.3	365	10	MMU22929	U22929 Mus musculus
27	291.4	80.2	418	6	AR026544	AR026544 Sequence
28	290.4	80.0	348	10	MMHCVR4	X75098 M. musculus
29	289.8	79.8	365	10	MMU22905	U22905 Mus musculus
30	289.8	79.8	365	10	MMU22909	U22909 Mus musculus
31	289.8	79.8	365	10	MMU22911	U22911 Mus musculus
32	289.8	79.8	365	10	MMU22926	U22926 Mus musculus
33	289.8	79.8	365	10	MMU22956	U22956 Mus musculus
34	289.8	79.8	365	10	MMU22957	U22957 Mus musculus
35	289.8	79.8	200065	2	AC073393	AC073393 Mus muscu
36	289.6	79.8	360	10	MMU22988	U22988 Mus musculus
37	289.2	79.7	326	10	MMU22986	U22986 Mus musculus
38	288.4	79.4	363	10	S82427	S82427 anti-paraqu
39	288.2	79.4	363	10	MMU22955	U22955 Mus musculus
40	287.8	79.3	1410	10	MMU421677	MMU421677 Mus muscu
41	285.6	78.7	357	10	S63186	S63186 Ig VH-anti-I
42	285	78.5	358	10	MMU22990	U22990 Mus musculus
43	285	78.5	330	10	MMU22975	U22975 Mus musculus
44	282.8	77.9	352	10	MMU22995	U22995 Mus musculus
45	281.8	77.6	363	10	MMU22907	U22907 Mus musculus

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

RESULT 1	
MMHCVR3	
LOCUS	MMHCVR3 360 bp mRNA linear ROD 23-FEB-199
DEFINITION	M.musculus (A.SW) mRNA for ASWBI antibody heavy chain variable region.
ACCESSION	X75097
VERSION	X75097.1 GI:414165
KEYWORDS	antibody; variable region; VH region.
SOURCE	Mus musculus.
ORGANISM	Mus musculus
	Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 360)
AUTHORS	Monestier,M.
TITLE	Direct Submision

JOURNAL Submitted (09-SEP-1993) M. Monestier, Center for Molecular Medicine and Immunology, One Bruce Street, Newark, NJ 07103-2763, USA

REFERENCE 2 (bases 1 to 360)

AUTHORS Monestier, M., Losman, M.J., Novick, K.E. and Arts, J.P.

TITLE Molecular analysis of mercury-induced antinuclear antibodies in H-2S mice

JOURNAL J. Immunol. 152 (2), 667-675 (1994)

PubMed 94110621

FEATURES

source location/Qualifiers

1..360

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="12"

/cell_line="ASMB1 hybridoma"

/cell_type="hybridoma"

1..360

/gene="VH ASMB1"

<1..>360

/gene="VH ASMB1"

/codon_start=1

/product="ASMB1 heavy chain variable region"

/protein_id="CA52988.1"

/db_xref="GI:414166"

/translation="QVTLKESGPGIILQPSOTLSLCSFSGFSLSGSGVSWIRPSG KGLEWLAHYMDKRNPSLSRLTSKDSRNQVFLKITSVDTRADTAHYCARVDG YVDAMWGQSTSVYSS"

<1..>360

/gene="VH ASMB1"

/product="ASMB1 heavy chain variable region"

BASE COUNT 82 a 95 c 89 g 94 t

ORIGIN

Query Match 87.2%; Score 316.6; DB 10; Length 360;

Best Local Similarity 93.9%; Pred. No. 1.1e-91;

Matches 341; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGACCCCTCCAGACCTCAGTCTG 60

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGACCCCTCCAGACCTCAGTCTG 60

61 ACTTGTCTTCTCTGGGTTTTCAGTACGACACTTGTGGTGGTGGTGGTGGTGGTGGT 120

61 ACTTGTCTTCTCTGGGTTTTCAGTACGACACTTGTGGTGGTGGTGGTGGTGGTGGT 120

121 CAGCTTCAAGAAAGGCTGTGAGTGTGCTGGACACATTTACTGGGATGTACAAGCCG 180

121 CAGCTTCAAGAAAGGCTGTGAGTGTGCTGGACACATTTACTGGGATGTACAAGCCG 180

121 CAGCTTCAAGAAAGGCTGTGAGTGTGCTGGACACATTTACTGGGATGTACAAGCCG 180

181 TATTAACCATCCCTGAAGAGCCGGCTTACAAATCTCCAAAGATACCTCCAGAACCA 240

181 TATTAACCATCCCTGAAGAGCCGGCTTACAAATCTCCAAAGATACCTCCAGAACCA 240

181 TATTAACCATCCCTGAAGAGCCGGCTTACAAATCTCCAAAGATACCTCCAGAACCA 240

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

301 GTCTCTTAAGTCCATGCTATGATGACTAGTGGGTCAGAGAACTCAGTACCGTCTCC 360

301 GTCTCTTAAGTCCATGCTATGATGACTAGTGGGTCAGAGAACTCAGTACCGTCTCC 360

298 GTGATGCTTACTACAGATGCTATGACTACTGCGGTCAAGAACTCAGTACCGTCTCC 357

361 TCA 363

358 TCA 360

RESULT 2

LOCUS AY090903 420 bp mRNA linear ROD 17-APR-2002

DEFINITION Mus musculus clone GN-2-M4 monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain mRNA, partial cds.

ACCESSION AY090903

VERSION AY090903.1 GI:20177160

KEYWORDS Mus musculus.

SOURCE Mus musculus.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 420)

AUTHORS Xu, H., Sharma, A., Chen, L., Harrison, C., Wei, Y., Cheng, A.S., Logan, J.S., Byrne, G.W. and Shama, A.

TITLE The structure of anti-Gal immunoglobulin genes in naive and transplanted Gal knockout mice

JOURNAL J. Immunol. 166 (1), 1817-1825 (2001)

PubMed 21605873

FEATURES

source location/Qualifiers

1..420

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="GN-2-M4"

/cell_type="hybridoma"

/note="generated in alpha-1,3-galactosyltransferase knockout mice"

<1..>420

/note="VDJ region"

/codon_start=1

/product="monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain"

/protein_id="AA012013.1"

/db_xref="GI:20177161"

/translation="QVTLKESGPGIILQPSOTLSLCSFSGFSLSGSGVSWIRPSG KGLEWLAHYMDKRNPSLSRLTSKDSRNQVFLKITSVDTRADTAHYCARVDG YVDAMWGQSTSVYSSSFHKLPSSTARRAPCHIR"

BASE COUNT 97 a 123 c 98 g 102 t

ORIGIN

Query Match 86.7%; Score 314.6; DB 10; Length 420;

Best Local Similarity 94.2%; Pred. No. 4.9e-91;

Matches 342; Conservative 0; Mismatches 9; Indels 12; Gaps 1;

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGACCCCTCCAGACCTCAGTCTG 60

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGACCCCTCCAGACCTCAGTCTG 60

61 ACTTGTCTTCTCTGGGTTTTCAGTACGACACTTGTGGTGGTGGTGGTGGTGGTGGT 120

61 ACTTGTCTTCTCTGGGTTTTCAGTACGACACTTGTGGTGGTGGTGGTGGTGGTGGT 120

121 CAGCTTCAAGAAAGGCTGTGAGTGTGCTGGACACATTTACTGGGATGTACAAGCCG 180

121 CAGCTTCAAGAAAGGCTGTGAGTGTGCTGGACACATTTACTGGGATGTACAAGCCG 180

121 CAGCTTCAAGAAAGGCTGTGAGTGTGCTGGACACATTTACTGGGATGTACAAGCCG 180

181 TATTAACCATCCCTGAAGAGCCGGCTTACAAATCTCCAAAGATACCTCCAGAACCA 240

181 TATTAACCATCCCTGAAGAGCCGGCTTACAAATCTCCAAAGATACCTCCAGAACCA 240

181 TATTAACCATCCCTGAAGAGCCGGCTTACAAATCTCCAAAGATACCTCCAGAACCA 240

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

241 TTCCCTCAAGATCAGAGTGTGACACTCGAGATACCTGACATCTACTGCTCGAAGG 300

301 GTCTCTTAAGTCCATGCTATGATGACTAGTGGGTCAGAGAACTCAGTACCGTCTCC 360

301 GTCTCTTAAGTCCATGCTATGATGACTAGTGGGTCAGAGAACTCAGTACCGTCTCC 360

300 -----ACCCACGCTATGACTACTGCGGTCAAGAACTCAGTACCGTCTCC 348

361 TCA 363

349 TCA 351

RESULT 3
LOCUS AX458152 426 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 15 from Patent WO0246237.
ACCESSION AX458152
VERSION AX458152.1 GI:21724902
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Basi, G., Saldanha, J. and Vednock, T.
TITLE Humanized antibodies that recognize beta amyloid peptide
JOURNAL Patent: WO 0246237-A 15 13-JUN-2002;
Neuralab Limited (BM) ; Wyeth (US)
FEATURES
source location/Qualifiers
1..426
/organism="Mus musculus"
/db_xref="taxon:10090"
1..>426
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD38347.1"
/db_xref="GI:21724903"
/translation="MDRLSSFLILIPAVYLISQATLKESGRLTSSGNGVSRNPQSG
GFSLSTSGMGVSRNPQSGKGLIEMIAHLYDDDKRNPRLTSSKRLTSSKRVFLK
ITSVDPADTATYICVRNPITPLVADMDWGQHSIVSS"
sig_peptide 1..57
BASE COUNT 94 a 119 c 101 g 112 t
ORIGIN
Query Match 85.9%; Score 311.8; DB 6; Length 426;
Best Local Similarity 92.4%; Pred. No. 4e-90; Mismatches 22; Indels 6; Gaps 1;
Matches 341; Conservative 0; Mismatches 22; Indels 6; Gaps 1;
QY 1 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGCTG 60
DB 58 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGCTG 117
QY 61 ACTGTCTCTCTCTGGGTTTTCAGTGACACTTGTGGTATGGGTGTGAGCTGATTGCA 120
DB 118 ACTGTCTCTCTCTGGGTTTTCAGTGACACTTGTGGTATGGGTGTGAGCTGATTGCT 177
QY 121 CAGCCTTCAGGAAGAGCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAAGCGC 180
DB 178 CAGCCTTCAGGAAGAGCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAAGCGC 237
QY 181 TATAACCCATCCCTGAAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACGAGTA 240
DB 238 TATAACCCATCCCTGAAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACGAGTA 297
QY 241 TTCTCTCAAGATACCAAGTGTGACACTCGAGATACCTCCAGCAATCTGCTGGAAG 300
DB 298 TTCTCTCAAGATACCAAGTGTGACACTCGAGATACCTCCAGCAATCTGCTGGAAG 357
QY 301 GTC-----TCTCTACAGCCTATGCTATGACATCTGGGGTCAAGAAACCTCAGTACC 354
DB 358 CCCATTACTCCGGTACTAGTCGATGCTATGACATCTGGGGTCAAGAAACCTCAGTACC 417
QY 355 GTCCTCCTCA 363
DB 418 GTCCTCCTCA 426
RESULT 4
LOCUS MMU22977 360 bp mRNA linear ROD 09-APR-1996
DEFINITION Mus musculus Cbl7 SCID immunoglobulin heavy chain V region mRNA,
clone 45-11h, partial cds.
ACCESSION U22977
VERSION U22977.1 GI:780556
KEYWORDS

SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Young, D. and Kearney, J. F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
source location/Qualifiers
1..360
/organism="Mus musculus"
/strain="Cbl7 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-11h"
/cell_type="lymphocyte"
/tissue_type="spleen"
1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AAA96358.1"
/db_xref="GI:780557"
/translation="QVTLKESGRLTSSGNGVSRNPQSG
KGLIEMIAHLYDDDKRNPRLTSSKRLTSSKRVFLKITSVDPADTATYICARVLL
GSSYFDYWGQDTTLTVSS"
CDS
BASE COUNT 84 a 97 c 87 g 92 t
ORIGIN
Query Match 84.1%; Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0%; Pred. No. 4.8e-88; Mismatches 26; Indels 3; Gaps 1;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGCTG 60
DB 1 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGCTG 60
QY 61 ACTGTCTCTCTCTGGGTTTTCAGTGACACTTGTGGTATGGGTGTGAGCTGATTGCA 120
DB 61 ACTGTCTCTCTCTGGGTTTTCAGTGACACTTGTGGTATGGGTGTGAGCTGATTGCT 120
QY 121 CAGCCTTCAGGAAGAGCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAAGCGC 180
DB 121 CAGCCTTCAGGAAGAGCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAAGCGC 180
QY 181 TATAACCCATCCCTGAAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACGAGTA 240
DB 181 TATAACCCATCCCTGAAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACGAGTA 240
QY 241 TTCTCTCAAGATACCAAGTGTGACACTCGAGATACCTCCAGCAATCTGCTGGAAG 300
DB 241 TTCTCTCAAGATACCAAGTGTGACACTCGAGATACCTCCAGCAATCTGCTGGAAG 300
QY 301 GTCCTCTACAGCCTATGCTATGACATCTGGGGTCAAGAAACCTCAGTACC 360
DB 301 GT---TCTAGGTAGTACTTGTGACTGCTGGGGTCAAGAAACCTCAGTACC 357
QY 361 TCA 363
DB 358 TCA 360
RESULT 5
LOCUS MMU22979 360 bp mRNA linear ROD 09-APR-1996
KEYWORDS

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-12h, partial cds.

ACCESSION U22979
VERSION U22979.1 GI:780560

KEYWORDS Mus musculus.

SOURCE Mus musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
1 (bases 1 to 360)

AUTHORS Young, D. and Kearney, J.F.

TITLE Ig SCID

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

PUBMED 7547707

REFERENCE 2 (bases 1 to 360)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

FEATURES
LOCATION/Qualifiers
1..360
/organism="Mus musculus"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-12h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA96360.1"
/db_xref="GI:780561"
/translation="QVTLKESGCGILOSSTLTSFSGFSSTSGMYSWIRQPSG
KGLEMLHIYDDDKRYNPSLKRSLTSLSKTSRNOVFLKITSVDATATYTCARRVL
GSSYFDWGGGTLTVSS"

CDS
84 a 98 c 87 g 91 t

BASE COUNT 84 a 98 c 87 g 91 t

ORIGIN

Query Match 84.1% Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0% Pred. No. 4.8e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAGTCTG 60
|||||
1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAGTCTG 60
|||||

61 ACTTGTCTTCTCTGCTGGGTTTTCAGTACGACACTTCTGTATGGGTGAGCTGGATTGCA 120
|||||
61 ACTTGTCTTCTCTGCTGGGTTTTCAGTACGACACTTCTGTATGGGTGAGCTGGATTGCA 120
|||||

121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAAGCCG 180
|||||
121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAAGCCG 180
|||||

181 TATAACCATCCCTGGAAGAGCCGGCTTACATCTCCAAGATACCTCCAGCAACAGGTA 240
|||||
181 TATAACCATCCCTGGAAGAGCCGGCTTACATCTCCAAGATACCTCCAGCAACAGGTA 240
|||||

241 TTCTCTCAAGATCACCACTGTGGACACTGAGATACCTCCACATCTACTGCTGCGAAG 300
|||||
241 TTCTCTCAAGATCACCACTGTGGACACTGAGATACCTCCACATCTACTGCTGCGAAG 300
|||||

301 GTCTCTTAAGTACCTGCTATGCTATGAGTACTAGGGGTGAAGAACCTCAGTCCGCTCC 360
|||||
301 GTCTCTTAAGTACCTGCTATGCTATGAGTACTAGGGGTGAAGAACCTCAGTCCGCTCC 360
|||||

361 TCA 363
|||
361 TCA 363
|||

358 TCA 360

RESULT 6
LOCUS MMU22994 360 bp mRNA linear ROD 09-APR-1996

DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-27h, partial cds.

ACCESSION U22994
VERSION U22994.1 GI:780590

KEYWORDS Mus musculus.

SOURCE Mus musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
1 (bases 1 to 360)

AUTHORS Young, D. and Kearney, J.F.

TITLE Ig SCID

JOURNAL Int. Immunol. 7 (5), 807-819 (1995)

MEDLINE 96053543

PUBMED 7547707

REFERENCE 2 (bases 1 to 360)

AUTHORS Young, D.C.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

FEATURES
LOCATION/Qualifiers
1..360
/organism="Mus musculus"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-27h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA96375.1"
/db_xref="GI:780591"
/translation="QVTLKESGCGILOSSTLTSFSGFSSTSGMYSWIRQPSG
KGLEMLHIYDDDKRYNPSLKRSLTSLSKTSRNOVFLKITSVDATATYTCARRVL
GSSYFDWGGGTLTVSS"

CDS
84 a 95 c 87 g 94 t

BASE COUNT 84 a 95 c 87 g 94 t

ORIGIN

Query Match 84.1% Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0% Pred. No. 4.8e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAGTCTG 60
|||||
1 CAGGTACTCTGAAAGAGTCTGGCCCTGGATATTGACGCCCTCCAGACCTCAGTCTG 60
|||||

61 ACTTGTCTTCTCTGCTGGGTTTTCAGTACGACACTTCTGTATGGGTGAGCTGGATTGCA 120
|||||
61 ACTTGTCTTCTCTGCTGGGTTTTCAGTACGACACTTCTGTATGGGTGAGCTGGATTGCA 120
|||||

121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAAGCCG 180
|||||
121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAAGCCG 180
|||||

181 TATAACCATCCCTGGAAGAGCCGGCTTACATCTCCAAGATACCTCCAGCAACAGGTA 240
|||||
181 TATAACCATCCCTGGAAGAGCCGGCTTACATCTCCAAGATACCTCCAGCAACAGGTA 240
|||||

241 TTCTCTCAAGATCACCACTGTGGACACTGAGATACCTCCACATCTACTGCTGCGAAG 300
|||||
241 TTCTCTCAAGATCACCACTGTGGACACTGAGATACCTCCACATCTACTGCTGCGAAG 300
|||||

301 GTCTCTTAAGTACCTGCTATGCTATGAGTACTAGGGGTGAAGAACCTCAGTCCGCTCC 360
|||||
301 GTCTCTTAAGTACCTGCTATGCTATGAGTACTAGGGGTGAAGAACCTCAGTCCGCTCC 360
|||||

DB 301 GT---CTAGTAGTAGTACTTGTACTGAGGCGCAGCACCCTCTACAGTCTCC 357
QY 361 TCA 363
DB 358 TCA 360

RESULT 7
MWU22992
LOCUS MWU22992 360 bp mRNA linear ROD 09-APR-1996
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-26h, partial cds.
ACCESSION U22992
VERSION U22992
KEYWORDS U22992.1 GI:780586
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young, D. and Kearney, J. F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PubMed 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

FEATURES
source location/Qualifiers
1..360
/organism="Mus musculus"
/strain="CB17 SCID"
/sub-species="domesticus"
/db_xref="taxon:10090"
/clone="45-26h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA96373.1"
/db_xref="GI:780587"
/translation="QVTLKESGPILQSSQTLSTLCSFSGSLSTSGMGVSWIRPQSG
KGLMLAIYWDGDRNPNPLSKSRILITSKDPSRQVFLKITSVDTADTATVYCARRAL
GSTYFDWGGCTTIVS"

CDS
1..360
/product="immunoglobulin heavy chain"
/protein_id="AA96373.1"
/db_xref="GI:780587"
/translation="QVTLKESGPILQSSQTLSTLCSFSGSLSTSGMGVSWIRPQSG
KGLMLAIYWDGDRNPNPLSKSRILITSKDPSRQVFLKITSVDTADTATVYCARRAL
GSTYFDWGGCTTIVS"

BASE COUNT 83 a 99 c 87 g 91 t
ORIGIN

Query Match 83.7%; Score 303.8; DB 10; Length 360;
Best Local Similarity 91.7%; Pred. No. 1.6e-87;
Matches 333; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 CAGGTACTCGAAGAGCTGCGCCCTGGATATGACGCCCTCCAGACCTCAGTCTG 60
DB 1 CAGGTACTCGAAGAGCTGCGCCCTGGATATGACGCCCTCCAGACCTCAGTCTG 60
QY 61 ACTGTCTCTCTCTGCGGTTTCACTGAGCACTTCTGATGAGGTGAGCTGATTCGA 120
DB 61 ACTGTCTCTCTCTGCGGTTTCACTGAGCACTTCTGATGAGGTGAGCTGATTCGT 120
QY 121 CAGCTTCAGGAAGAGGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAGCGC 180
DB 121 CAGCTTCAGGAAGAGGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAGCGC 180
QY 181 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGAACAGGTA 240
DB 181 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGAACAGGTA 240
QY 241 TTCTCAAGATCACACAGTGTGAGACACTGAGATACCTGACATACCTACTGTGTCGAAG 300

DB 241 TTCTCAAGATCACACAGTGTGAGACACTGAGATACCTGACATACCTACTGTGTCGAAG 300
QY 301 GTCTCTACTGCGCTATGATGACTACTGAGGCTCAGGAACCTCAGTACCGCTCTCC 360
DB 301 G---CTTAGAGTAGTACTTGTACTGAGGCGCAGCACCCTCTACAGTCTCC 357

QY 361 TCA 363
DB 358 TCA 360

RESULT 8
E07584
LOCUS E07584 366 bp RNA linear PAT 29-SEP-1997
DEFINITION Gene fragment coding the variable region in the heavy chain.
ACCESSION E07584
VERSION E07584.1 GI:2175719
KEYWORDS JP 1994141885-A/1.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 366)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eda, Y., Nagatomi, K., Shiosaki, K., Maeda, H., Kurumi, K. and
Tokiyoshi, Y.
TITLE MONOCLONAL ANTIBODY
JOURNAL Patent: JP 1994141885-A 1 24-MAY-1994;
CHEMO SERO THERAPEUT RES INST
OS Mus sp. (mouse)
PN JP 1994141885-A/1
PD 24-MAY-1994
PF 05-NOV-1992 JP 1992322476
PI ED A YASUYUKI, NAGATOMI KIYOSHI, SHIOSAKI KOUICHI, PI MAEDA
HIROAKI,
PI KURUMI KAZUHIKO, TOKIYOSHI YUKIO
PC C12P21/08.C07K15/28//C12M15/06.C12M15/13.C12M15/62.G01N33/569,
PC G01N33/577.
PC (C12P21/08.C12K1:91);
CC strandedness: Double;
CC topology: linear;
FH key Location/Qualifiers
FH source 1..366
FT Location/Qualifiers
1..366
/organism="Mus sp."
/db_xref="taxon:10095"

BASE COUNT 85 a 98 c 84 g 99 t
ORIGIN

Query Match 83.6%; Score 303.6; DB 6; Length 366;
Best Local Similarity 91.3%; Pred. No. 1.8e-87;
Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTACTCGAAGAGCTGCGCCCTGGATATGACGCCCTCCAGACCTCAGTCTG 60
DB 1 CAGGTACTCGAAGAGCTGCGCCCTGGATATGACGCCCTCCAGACCTCAGTCTG 60
QY 61 ACTGTCTCTCTCTGCGGTTTCACTGAGCACTTCTGATGAGGTGAGCTGATTCGA 120
DB 61 ACTGTCTCTCTCTGCGGTTTCACTGAGCACTTCTGATGAGGTGAGCTGATTCGT 120
QY 121 CAGCTTCAGGAAGAGGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAGCGC 180
DB 121 CAGCTTCAGGAAGAGGTCTGAGTGGCTGGCAGACATTTACTGGATGATGACAGCGC 180
QY 181 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGAACAGGTA 240
DB 181 TATTAACCATCCCTGGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGAACAGGTA 240
QY 241 TTCTCAAGATCACACAGTGTGAGACACTGAGATACCTGACATACCTACTGTGTCGAAG 300

Db	241	TTTCCTCAAGATCACCACCTGTGACACTGCAGATCTGTGCACATCTACTGTGCTCGAAGG	300
Qy	301	G---TTCCTCTACTGCTCTATGCTATGACACTTGGGGTCAAGAACCTCAGTACCCTC	357
Db	301	GTCTTCTATGCTAACTCCGATTTTATGACACACTGGGGTCAAGAACCTCAGTACCCTC	360
Qy	358	TCCTCA	363
Db	361	TCCTCA	366

RESULT	9
MU022981	
LOCUS	
DEFINITION	MMU22981 360 bp mRNA linear ROD 09-APR-1996
ACCESSION	U22981 clone 45-13h, partial cds.
VERSION	U22981.1 GI:780564

ORGANISM	REFERENCE	AUTHORS	TITLE
<i>Mus musculus</i>			Sequence analysis and antigen binding characteristics of Ig SCID
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
1 (Passes 1 to 360)			
Young, D. and Kearney, J. F.			

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITL
JOURNAL

Int. Immunol. 7 (5), 807-819 (1995)
96053543
7547707
2 (bases 1 to 360)
Young, D. C.
Direct Submission
Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA

```

FEATURES
source      Location/Qualifiers
            1..360
            /organism="Mus musculus"
            /strain="CB17 SCID"
            /sub_species="domesticus"
            /db_xref="taxon:10090"
            /clone="45-13h"
            /cell_type="lymphocyte"
            /tissue_type="spleen"
            <1..>360

```

```

/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA06362.1"
/db_xref="GI:780565"
/translation="OVLKESGSGITLQSOTLSTCSFSPSLSTSCMGYSWYRPPSC
KGLGMLHYAMDCKRNKPSLKRITLSTKTSRNOVYLRITSDTADTATYYCARRAL
GSTFEDYMGGGITLVNS"

```

Query Match	82.8%	Score 300.6	DB 10	Length 360
Best Local Similarity	91.2%	Pred. No. 1.7e-85		
Matches	331	Conservative	0	Mismatches 23
			Indels	3
			Gaps	1
QY	1	CAGGTTACTGTGAAGAAGTGTGGCCCTGGATATTGACAGCCCTCCAGACCCCTCAGTGTG	60	
Db	1	CAGGTTACTGTGAAGAAGTGTGGCCCTGGATATTGACAGTCTCCAGACCCCTCAGTGTG	60	
QY	61	ACTTGTTCTTCTCTGGGTTTCACTGAGCACTTCTGATAGGCTGAGCTGATTCGA	120	
Db	61	ACTTGTTCTTCTCTGGGTTTCACTGAGCACTTCTGATAGGCTGAGCTGATTCGT	120	
QY	121	CAGGCTTCAGGAAGGCTGGAGTGGGTGACACATTTACTGSGGATGATGACAAGGCG	180	
Db	121	CAGGCTTCAGGAAGGCTGGAGTGGGTGACACATTTACTGSGGATGATGACAAGGCG	180	

QY	181	TATTAACCCATCCCTGTAAGAGCCGGGTTCAATCTCCAAAGATTAACCTCAGACAAACAGSTA	240
QY	181	TATTAACCCATCCCTGTAAGAGCCGGGTTCAATCTCCAAAGATTAACCTCAGACAAACAGSTA	240
Db	181	TATTAACCCATCCCTGTAAGAGCCGGGTTCAATCTCCAAAGATTAACCTCAGACAAACAGSTA	240
QY	241	TTTCCTCAAGATCACACAGTGTGACACTCGAGATTAATCTGCACATCTACTGTCTCGAAGG	300
Db	241	TTTCCTCAAGATCACACAGTGTGACACTCGAGATTAATCTGCACATCTACTGTCTCGAAGG	300
QY	241	TTTCCTCAAGATCACACAGTGTGACACTCGAGATTAATCTGCACATCTACTGTCTCGAAGG	300
Db	241	TTTCCTCAAGATCACACAGTGTGACACTCGAGATTAATCTGCACATCTACTGTCTCGAAGG	300
QY	301	GTTCTCTCTAATCGCTTAATCTGTGACATTAATCTGAGGATCAAGAACCTTAGTACACCGTCTCC	360
Db	301	GTTCTCTCTAATCGCTTAATCTGTGACATTAATCTGAGGATCAAGAACCTTAGTACACCGTCTCC	360
QY	301	GTTCTCTCTAATCGCTTAATCTGTGACATTAATCTGAGGATCAAGAACCTTAGTACACCGTCTCC	360
Db	301	GTTCTCTCTAATCGCTTAATCTGTGACATTAATCTGAGGATCAAGAACCTTAGTACACCGTCTCC	360
QY	361	TCA	363
Db	361	TCA	363
QY	358	TCA	360
Db	358	TCA	360

RESULT	10
MMU23010	
LOCUS	
DEFINITION	Mus musculus Cbl7 SCID immunoglobulin heavy chain V region mRNA,
ACCESSION	U23010
VERSION	U23010.1 GI:780622

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognata; Muridae; Murine; Mus
1 (Phases 1 to 360)
Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice
Int. Immunol. 7 (5), 807-819 (1995)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Int. Immunol. 7 (5), 807-819 (1995)
96053543
7547707
2 (bases 1 to 360)
Young D.C.
Direct Submission
Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.13,
Houston, TX 77030, USA

```

FEATURES
SOURCE
location/Qualifiers
1..360
/organism="Mus musculus"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-6h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
CDS

```

BASE COUNT	83 a	99 c	87 g	91 t
ORIGIN	/codon_start=1 /product="immunoglobulin heavy chain" /protein_id="AA055401.1" /db_xref="GI:780623" /translation="QVTLKEGPGCIIDSSQTLSTFCFSELSLSCMGVSMINQPSG KGLMELHITWDEPKRINPSLKSRLTISKDISKQVFLRITVDTADTAIYCCARRAL GSYTFDEWGGGTYLLVSS"			

	Query Match	82.8%	Score 300.6;	DB 10;	Length 360;
	Best Local Similarity	91.2%;	Pred. No. 1.7e-86;		
	Matches 331;	Conservative 0;	Mismatches 29;	Indels 3;	Gaps 1;
Oy	1 CAGGTTACTCTGAAGAAGTCTGGGCCCTGGGATATTGCAGCCCTCCACAGCCTCAGTCGTG	60			
Db	1 CAGGTTACTCTGAAGAAGTCTGGGCCCTGGGATATTGCAGTCCTCCAACACCTCAGTCGTG	60			
Oy	61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTTCTGGTATATGGGTTGAGCGATTCGA	120			
Db	61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTTCTGGTATATGGGTTGAGCGATTCGT	120			

QY 121 CAGCTTCAGGAAGGGCTGAGAGTGGCTGGACACATTCTATGGGATGACAGGCG 180
|||||
DB 121 CAGCTTCAGGAAGGGCTGAGAGTGGCTGGACACATTCTATGGGATGACAGGCG 180
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAAATCTCCAGAGATACCTCCAGCAACAGGTA 240
|||||
DB 181 TATAACCCATCCCTGAAGAGCGGCTTACAAATCTCCAGAGATACCTCCAGCAACAGGTA 240
QY 241 TTCCTCAAGATCACCAGTGTGACACTGCAATATCTGCCACATATCTACTGTGCTGGAAG 300
|||||
DB 241 TTCCTCAAGATCACCAGTGTGACACTGCAATATCTGCCACATATCTACTGTGCTGGAAG 300
QY 301 GTCCTCTAAGTACCTATGCTATGAGTACTGGGGTCAAGGAACCTGATCAGCGTCGCC 360
|||||
DB 301 GTCCTCTAAGTACCTATGCTATGAGTACTGGGGTCAAGGAACCTGATCAGCGTCGCC 360
QY 361 TCA 363
|||
DB 358 TCA 360

RESULT 11
MMU23013 360 bp mRNA linear ROD 20-SEP-2001
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-8h, partial cds.
ACCESSION U23013
VERSION U23013.1 GI:780628
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Young, D. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submision
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
source location/Qualifiers
1..360
/organism="Mus musculus"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-8h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA65404.1"
/db_xref="GI:780629"
/translation="QVTLKESGPILOSQTLSTLCSFSGFSLSTSGMGVSWIRPSS
KGLMLTHIYWDGDKRYNPSLKSRLTISKDSRNQVFLRITSVDTADTATYYCARRAL
GSTFDYWGQSTLTLYSS"

BASE COUNT 83 a 99 c 87 g 91 t
ORIGIN
Query Match 82.8%; Score 300.6; DB 10; Length 360;
Best Local Similarity 91.2%; Pred. No. 1.7e-86;
Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
1 CAGCTTACTCTGAAGAAGTCTGGCCCTGGATATTGACAGCTCCAGACCCCTCAGTCTG 60
|||||

DB 1 CAGCTTACTCTGAAGAAGTCTGGCCCTGGATATTGACAGCTCCAGACCCCTCAGTCTG 60
QY 61 ACTGTCTCTCTCTGTTGGTTTTCACACTGAGCACTTCTGTAATGGGTGAGCTGATTCGA 120
|||||
DB 61 ACTGTCTCTCTCTGTTGGTTTTCACACTGAGCACTTCTGTAATGGGTGAGCTGATTCGT 120
QY 121 CAGCTTCAGGAAGGGCTGAGAGTGGCTGGACACATTCTATGGGATGACAGGCG 180
|||||
DB 121 CAGCTTCAGGAAGGGCTGAGAGTGGCTGGACACATTCTATGGGATGACAGGCG 180
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAAATCTCCAGAGATACCTCCAGCAACAGGTA 240
|||||
DB 181 TATAACCCATCCCTGAAGAGCGGCTTACAAATCTCCAGAGATACCTCCAGCAACAGGTA 240
QY 241 TTCCTCAAGATCACCAGTGTGACACTGCAATATCTGCCACATATCTACTGTGCTGGAAG 300
|||||
DB 241 TTCCTCAAGATCACCAGTGTGACACTGCAATATCTGCCACATATCTACTGTGCTGGAAG 300
QY 301 GTCCTCTAAGTACCTATGCTATGAGTACTGGGGTCAAGGAACCTGATCAGCGTCGCC 360
|||||
DB 301 GTCCTCTAAGTACCTATGCTATGAGTACTGGGGTCAAGGAACCTGATCAGCGTCGCC 360
QY 361 TCA 363
|||
DB 358 TCA 360

RESULT 12
MMU23004 361 bp mRNA linear ROD 20-SEP-2001
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-3h, partial cds.
ACCESSION U23004
VERSION U23004.1 GI:780610
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Young, D. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 361)
AUTHORS Young, D.C.
TITLE Direct Submision
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
source location/Qualifiers
1..361
/organism="Mus musculus"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-3h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>361
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA65395.1"
/db_xref="GI:780611"
/translation="QVTLKESGPILOSQTLSTLCSFSGFSLSTSGMGVSWIRPSS
KGLMLTHIYWDGDKRYNPSLKSRLTISKDSRNQVFLRITSVDTADTATYYCARRAL
GSTFDYWGQSTLTLYSS"

BASE COUNT 83 a 99 c 88 g 91 t
ORIGIN
Query Match 82.8%; Score 300.6; DB 10; Length 361;

```

/product="immunoglobulin heavy chain"
/protein_id="AA65390.1"
/db_xref="GI:780601"
/translation="QVTLKSGPGILQSSQTLSTLCFSGFSLSTSGKGVMIWIPSG
/GLEMLHIWDDGDKRNPKLSKRLTISDTSNVOYFLRITVSDPADRIATYYCARRAL

```

```

FT      /product='inhibitor of binding of IL-6 to its
FT      receptor'
FEATURES
source  Location/Qualifiers
1..738
        /organism="unidentified"
        /db_xref="taxon:32644"

```

BASE COUNT 187 a 189 c 180 g 182 t
ORIGIN

Query Match 82.4%; Score 299.2; DB 6; Length 738;
Best Local Similarity 90.1%; Pred. No. 5,1e-86;
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 367 CAGGTCAAACTCGAGAGCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 426
QY 61 ACTGTCTCTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGATTCGA 120
DB 427 ACTGTCTCTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGATTCGT 486
QY 121 CAGCTTCAGAAAGAGGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCC 180
DB 487 CAGCTTCAGAAAGAGGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAAAC 546
DB 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGATACCTCCAGACACAGSTA 240
DB 547 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGATACCTCCAGACACAGSTA 606
QY 241 TTCCTCAAGATCACCAGTGTGAGACACTGAGATACCTGACATCTGCTCGAAG- 299
DB 607 TTCCTCAAGATCACCAGTGTGAGACACTGAGATACCTGACATCTGCTCGAAGA 666
QY 300 -----GGTCTCTTACTGCTATGCTATGAGACTGAGGCTCAAGAACTCAGTC 351
DB 667 AGTCTCTATGTTATTTGGGGGAGCTATGCTATGAGACTGAGGCTCAAGAACTCAGTC 726
QY 352 ACCGTCCTCTCA 363
DB 727 ACCGTCCTCTCA 738

RESULT 15

LOCUS 145910 738 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5639455.
ACCESSION 145910
VERSION 145910.1 GI:2469875
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 738)
AUTHORS Shimamura,T., Nakazawa,H. and Hamuro,J.
TITLE Immunosuppressant
JOURNAL Patent: US 5639455-A 6 17-JUN-1997;
FEATURES
SOURCE Location/Qualifiers
1..738
/organism="unknown"

BASE COUNT 187 a 189 c 180 g 182 t
ORIGIN

Query Match 82.4%; Score 299.2; DB 6; Length 738;
Best Local Similarity 90.1%; Pred. No. 5,1e-86;
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 367 CAGGTCAAACTCGAGAGCTGGCCCTGGATATTGACGCCCTCCAGACCCCTCAGTCTG 426
QY 61 ACTGTCTCTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGATTCGA 120
DB 427 ACTGTCTCTCTCTGGGTTTTCACCTGACACTTCTGTATGGGTGAGCTGATTCGT 486
QY 121 CAGCTTCAGAAAGAGGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCC 180
DB 487 CAGCTTCAGAAAGAGGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAAAC 546
QY 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGATACCTCCAGACACAGSTA 240

DB 547 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGATACCTCCAGACACAGSTA 606
QY 241 TTCCTCAAGATCACCAGTGTGAGACACTGAGATACCTGACATCTGCTCGAAG- 299
DB 607 TTCCTCAAGATCACCAGTGTGAGACACTGAGATACCTGCTGCTCGAAGA 666
QY 300 -----GGTCTCTTACTGCTATGCTATGAGACTGAGGCTCAAGAACTCAGTC 351
DB 667 AGTCTCTATGTTATTTGGGGGAGCTATGCTATGAGACTGAGGCTCAAGAACTCAGTC 726
QY 352 ACCGTCCTCTCA 363
DB 727 ACCGTCCTCTCA 738

Search completed: July 10, 2003, 22:48:51
Job time : 1859 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 22:13:44 ; Search time 51 Seconds
(without alignments)
2182.817 Million cell updates/sec

Title: US-09-759-112a-5
Perfect score: 363
Sequence: 1 caggttactctgaagaagtc.....cctcagtcacgcgtctctca 363

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2-6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2-6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2-6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2-6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2-6/ptodata/1/ina/PTUTUS.COMB.seq: *
6: /cgn2-6/ptodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	313.4	86.3	483	2	US-08-483-636-3
2	313.4	86.3	483	2	US-08-483-632-3
3	311.8	85.9	423	2	US-08-483-636-9
4	311.8	85.9	423	2	US-08-483-632-9
5	299.2	82.4	738	1	US-08-197-834-6
6	296.4	81.7	417	5	PCT-US95-07372-9
7	291	80.2	418	2	US-08-535-501A-28
8	291	80.2	418	3	US-09-205-231-28
9	261.8	72.1	462	1	US-08-436-463-1
10	250.8	69.1	812	1	US-08-408-133-1
11	250.8	69.1	812	1	US-08-454-683-1
12	250.8	69.1	812	2	US-08-116-778E-16
13	250.8	69.1	812	2	US-08-454-680-1
14	250.8	69.1	812	2	US-08-438-562-16
15	250.8	69.1	812	2	US-08-483-528B-16
16	250.8	69.1	812	2	US-08-673-799C-16
17	250.8	69.1	812	4	US-09-393-385B-16
18	250.8	69.1	812	4	US-09-225-332B-1
19	190.6	52.5	423	2	US-08-345-321-9
20	190.2	52.4	613	3	US-08-345-809A-5
21	185.4	51.1	418	2	US-08-553-501A-58
22	185.4	51.1	418	2	US-09-205-231-58
23	185.4	51.1	1607	3	US-09-049-672A-14
24	183.8	50.6	418	2	US-08-553-501A-60
25	183.8	50.6	418	3	US-09-205-231-60
26	181.2	49.9	546	3	US-08-545-809A-26
27	172.6	47.5	630	3	US-08-545-809A-10

28	171	47.1	423	2	US-08-483-636-11	Sequence 11, Appl
29	171	47.1	423	2	US-08-483-632-11	Sequence 11, Appl
30	165	45.5	714	4	US-09-142-974B-2	Sequence 2, Appl
31	165	45.5	1173	4	US-09-142-974B-4	Sequence 4, Appl
32	163.2	45.0	378	1	US-08-488-376-15	Sequence 15, Appl
33	163.2	45.0	378	2	US-08-634-223-15	Sequence 15, Appl
34	163.2	45.0	378	2	US-08-634-224-15	Sequence 15, Appl
35	163.2	45.0	378	2	US-08-634-400-15	Sequence 15, Appl
36	163.2	45.0	378	2	US-08-635-878-15	Sequence 15, Appl
37	163.2	45.0	378	2	US-08-770-057-15	Sequence 15, Appl
38	163.2	45.0	378	4	US-09-335-697B-15	Sequence 15, Appl
39	163.2	45.0	378	4	US-09-335-697B-15	Sequence 15, Appl
40	163.2	45.0	1428	1	US-08-488-376-19	Sequence 19, Appl
41	163.2	45.0	1428	2	US-08-634-223-19	Sequence 19, Appl
42	163.2	45.0	1428	2	US-08-634-224-19	Sequence 19, Appl
43	163.2	45.0	1428	2	US-08-634-400-19	Sequence 19, Appl
44	163.2	45.0	1428	2	US-08-635-878-19	Sequence 19, Appl
45	163.2	45.0	1428	2	US-08-770-057-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-3
Sequence 3, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P.O. Box 1539 / UW220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50166-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
US-08-483-636-3

Query Match 86.3%; Score 313.4; DB 2; Length 483;
Best Local Similarity 91.5%; Pred. No. 5.8e-99;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTTGAGCCCTCCAGACCCCTAGCTG 60
DB 121 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTTGAGCCCTCCAGACCCCTAGCTG 180
QY 61 ACTTGTTCTTCTCTCTGGGTTTTCACAGCACTTCTGTAAGGTTGAGCTGATTCGA 120
DB 181 ACTTGTTCTTCTCTCTGGGTTTTCACAGCACTTCTGTAAGGTTGAGCTGATTCGT 240
QY 121 CAGCCTTCAGGAAAGGCTGCGAGTGGCTGGCACACATTTACTGGATGATGACACGCC 180
DB 241 CAGCCTTCAGGAAAGGCTGCGAGTGGCTGGCACACATTTACTGGATGATGACACGCC 300
QY 181 TATTAACCCATCCCTGGAAGAGCCGGCTGACATCTCCAAAGATATCTCCACCAACAGGTA 240
DB 301 TATTAACCCATCCCTGGAAGAGCCGGCTGACATCTCCAAAGATATCTCCACCAACAGGTA 360
QY 241 TTCCCTCAAGATCACACAGTGTGACACTGACATCTCCAAAGATATCTCCACCAACAGGTA 300
DB 361 TTCCCTCAAGATCACACAGTGTGACACTGACATCTCCAAAGATATCTCCACCAACAGGTA 420
QY 301 GTCTCTCAAGTCCCTATGCTATGAGACTACTGGGGTCAAGAACCTGACCGCTCC 360
DB 421 GAGACTGTGTTCTACTGTGACTGATGTCTGGGGCCGAGGACACGCTCAGCTCTCC 480
QY 361 TCA 363
DB 481 TCA 483

RESULT 2

US-08-483-632-3
Sequence 3, Application US/08483632
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
US-08-483-632-3.

Query Match 86.3%; Score 313.4; DB 2; Length 483;
Best Local Similarity 91.5%; Pred. No. 5.8e-99;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTTGAGCCCTCCAGACCCCTAGCTG 60
DB 121 CAGGTTACTGTAAGAGTCTGGCCCTGGGATATTTGAGCCCTCCAGACCCCTAGCTG 180
QY 61 ACTTGTTCTTCTCTCTGGGTTTTCACAGCACTTCTGTAAGGTTGAGCTGATTCGA 120
DB 181 ACTTGTTCTTCTCTCTGGGTTTTCACAGCACTTCTGTAAGGTTGAGCTGATTCGT 240
QY 121 CAGCCTTCAGGAAAGGCTGCGAGTGGCTGGCACACATTTACTGGATGATGACACGCC 180
DB 241 CAGCCTTCAGGAAAGGCTGCGAGTGGCTGGCACACATTTACTGGATGATGACACGCC 300
QY 241 TTCCCTCAAGATCACACAGTGTGACACTGACATCTCCAAAGATATCTCCACCAACAGGTA 300
DB 301 TATTAACCCATCCCTGGAAGAGCCGGCTGACATCTCCAAAGATATCTCCACCAACAGGTA 360
QY 301 GTCTCTCAAGTCCCTATGCTATGAGACTACTGGGGTCAAGAACCTGACCGCTCC 360
DB 421 GAGACTGTGTTCTACTGTGACTGATGTCTGGGGCCGAGGACACGCTCAGCTCTCC 480
QY 361 TCA 363
DB 481 TCA 483

RESULT 3

US-08-483-636-9
Sequence 9, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA

Query Match	95.9%	Score 311.8	DB 2	Length 423
Best Local Similarity	91.2%	Pred. No. 1.9e-98		
Matches 331:	Conservative 0	Mismatches 32	Indels 0	Gaps 0
QY	1	CAGGTTACTCTGAAAGAGCTGCGCCCTGGATATTGACAGCCCTCCAGACCCCTCAGTCTG	60	
DB	61	CAGGTTACCCCTGAAAGAGCTGCGCCCTGGATATTGACAGCCCTCCAGACCCCTCAGTCTG	120	
QY	61	ACTGTTCCTTCTCGGGTTTTCACGTAGACACTTCGTATGATGGGTGAGCTGAGTTCGA	120	
DB	121	ACTGTTCCTTCTCTGGGTTTTCACGTAGACACTTCGTATGATGGGTGAGCTGAGTTCGT	180	
QY	121	CAGCCTTCAGGAAAGGCTGTGAGTGCCTGCACACATTTCAGTGGATGATGACAAGCCG	180	
DB	181	CAGCCTTCAGGAAAGGCTGTGAGTGCCTGCACACATTTCAGTGGATGATGACAAGCCG	240	
QY	181	TATTAACCATCCCTGGAAGAGCCGGTTTCAATCTTCACAGAGATACCTCCAGCAACCAAGTA	240	
DB	241	TATTAACCATCCCTGGAAGAGCCGGTTCAAAATCTTCAAGGATACCTCCAGCAACCAAGTA	300	
QY	241	TTTCCTCAAGATCACCAGTGTGGACACTGAGATTAATGCCACATTAATAGTGTCTCGAAGG	300	
DB	301	TTTCCTCAAGATCACCAGTGTGGACACTGAGATTAATGCCACATTAATAGTGTCTCGAAGA	360	
QY	301	GTCCTCTCACTAGCCTATGCTATGAGACTACACTGAGGCTCAAGGAACCTCACTACCGTCTCC	360	
DB	361	GAGACTGTGTTCTACTGTGTAATCTGATGATCTGGGGGCGAGGACCAACGGCTACCGCTTCC	420	
QY	361	TCA 363		
DB	421	TCA 423		

RESULT 4
US-08-483-632-9

```

Sequence 9 Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TITL OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESS: Smithkline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
US-08-483-632-9

Query Match 85.9%; Score 311.8; DB 2; Length 423;
Best Local Similarity 91.2%; Pred. No. 1.9e-98;
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0

QY 1 CAGGTACTCTGGAAGAGTCTGCGCCCTGGGATATTGACAGCCCTCCCAAGCCTCAAGTCTG 60
Db 61 CAGGTATCCCTGGAAGAGTCTGCGCCCTGGGATATTGACAGCCCTCCCAAGCCTCAAGTCTG 120
QY 61 ACTGTTCTTCTCTCGGGTTTTCACCTGAGCACTTCTGGATGATGGTGTGAGTGGATTCGA 120
Db 121 ACTGTTCTTCTCTCGGGTTTTCACCTGAGCACTTCTGGATGATGGTGTGAGTGGATTCGT 180
QY 121 CAGCCTTCAGGAAGGCTCTGAGATGCTGGCACACATTTACTTGGGATGATGACAAGCGC 180
Db 181 CAGCCTTCAGGAAGGCTCTGAGATGCTGGCACACATTTACTTGGGATGATGACAAGCGC 240
QY 181 TATTAACCATCTCCCTGGAAGAGCCGGCTTTCATATCTTCAGAGGATACTCCAGCACCAAGTA 240
Db 241 TATTAACCATCTCCCTGGAAGAGCCGGCTTTCATATCTTCAGAGGATACTCCAGCACCAAGTA 300

```

OY 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 60
||||| - - - - -
Db 367 CAGGCTAAACTCGAGAGAGTCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 428

```

; NAME/KEY: misc_feature
; LOCATION: 1..57
; OTHER INFORMATION: /note="Signal peptide encoded by
; OTHER INFORMATION: nucleotides 1 through 57."

```



```

:      FEATURE:
:      NAME/KEY:  misc_feature
:      LOCATION:  58..417
:      OTHER INFORMATION:  /note="Mature peptide encoded by
:      OTHER INFORMATION:  nucleotides 58 through 417."
PCT-US95-07372-9

```

Query Match	81.7%	Score 296.4;	DB 5;	Length 417;
Best Local Similarity	90.6%;	Pred. No. 4.1e-93;		
Matches 328;	Conservative 0;	Mismatches 31;	Indels 3;	Gaps 1.

QY	1	CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTGCAGCCCTCCACAGCCTCAGTCTG	60
Db	58	CAGGTACTCTGAAAGAGCTGGCCCTGGGATATTGCAGCCCTCCACAGCCTCAGTCTG	117
QY	61	ACTGTGTCCTCTCTGGGTTTTCACTAGACACTTCTGGTATNGGCTGAGCTGGATTGGA	120
Db	118	ACTGTGTCCTCTCTGGGTTTTCACTAGAGACTTCTGGTATNGGCTGATGGCTGGATTGCT	177
	121	CAGCCTTCAGGAAAGGCTCTGGAGTGTGCTGGCAGCACATTTACTGGGATGATGACAAGCC	180
	178	CACCCCTTCAGGGAAGGCTCTGGAGTGTGCTGGCAGCACATTTGGTGGGATGATGACAAGCC	237
QY	181	TATATACCACATCCCTGAGAGCCGGGCTTAATCTCCAGAGATACCTCCAGAACACAGGTA	240
Db	238	TATATACCACATCCCTGAGAGCCGAGCTGATTAATCTCCAGAGATACCTCCAGGAAACAGGTA	297
QY	241	TTCCTCAAGTACCCAGTGTGGACACTCGAGATTACTGGCACATACTACTGTCTCGAAG	300
Db	298	TTCCTCAAGTGTCCGAGTGTGGACACTCGAGATTACTGGCACATACTACTGTCTCGAATG	357
QY	301	GTCCTCTCTAAGCTATGCTATGGACTATGGGCTCAAGGAACCTCAGTCACCGTCTCC	360
Db	358	ATGATG---GATTACAGACGCTATGGACTACTGGGCTCAAGGAACCTCAGTCACCGTCTCC	414
QY	361	TC	362
Db	415	TC	416

US-RESULT 7
US-08-553-501A-28
Sequence 28. Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSOCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuchi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMANN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 base pairs
ENCODING: 125 amino acids

NAME/KEY: CDS
LOCATION: 1..417
FEATURE:

NAME/KEY: mat_peptide
LOCATION: 1..417

Query Match	80.28;	Score 291;	DB 2;	Length 418;
Best Local Similarity	89.5%;	Pred. No. 3.1e-91;		
Matches 325;	Conservative 0;	Mismatches 35;	Indels 3;	Gaps 1.

QY	117	58	CAGGTACTCTGMAAGACTGTGGCCCTGGGATTTGCAAGCCCTCCAGACCTTAAGTCTG	117
Db				
QY	120	61	ACTGTGTCCTTCTCTGGGTTTTCACTGAGCACATTCGTGATGGGTTGAGCTGGATTGCA	120
Db				
QY	187	118	ACTGTGTCCTTCTCTGGTTTTTCACATGAACACTTCTGTATGACCGTAGCTGGATTTCGT	177
Db				
QY	237	121	CAGCCTTCAGGAAAGGGTCTGAGTGGCTGGGCACACATTTACTGGGATGATGACAAACGC	187
Db				
QY	240	178	CAGCCTTCAGGGAAGGGTCTGGAAGTGGCTGGGCACACATTTGGTGGAAAGATTAAGTAC	237
Db				
QY	248	181	TATTAACCCATCCCTGGAAGACCGGCTTTCATATCTCCAAGATTAACCTCCAGAACACAGTA	248
Db				
QY	297	238	TATTAACCCAGCCCTGAAAGGCGCGCTCAACAATCTCCAAAGGATTAACCTCCAAACACAGTA	297
Db				
QY	300	241	TTCCCTCAAGATCACCAAGTGTGGACACTCGAGATTAATGCCACATTACTATGTGTCGAAG	300
Db				
QY	357	298	TTCCCTCAAGTGGCCAGTGTGGTCACTCGAGATTAATGCCACATTACTATGTGTCGAATG	357
Db				
QY	366	301	GTCTCTCTAATGCTATGCTATGCACTAATGAGGCTCAAGAACCTCAAGTACCGCTCC	366
Db				
QY	414	358	GAGGAT---TAGAGACAGACGTATGCACTAATGCGGTCAAGGAACCTCAGTACCGCTCC	414
Db				
QY	363	361	TCA	
Db				
QY	417	415	TCA	
Db				

RESULT 8
US-09-205-231-28
Sequence 28, Application US/09205231
Patent No. 6121423
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMANA
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,231
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..417
NAME/KEY: mat_peptide
LOCATION: 1..417
US-09-205-231-28

Query Match 80.2%; Score 291; DB 3; Length 418;
Best Local Similarity 89.5%; Pred. No. 3.1e-91;
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 60
DB 58 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 117
QY 61 ACTTGTCTTCTCTGGGTTTTCAGTACACTTCTGTATGGGTGTGAGCTGGATTGCA 120
DB 118 ACTTGTCTTCTCTGGGTTTTCAGTACACTTCTGTATGGGTGTGAGCTGGATTGCGT 177
QY 121 CAGCCTTCAGGAAAGGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAAAGCGC 180
DB 178 CAGCCTTCAGGAAAGGCTGAGTGGCTGGCAGACATTTGGTGGATGATGATTAATAC 237
QY 181 TATAACCATCCCTGAAGAGCCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 240
DB 238 TATAACCATCCCTGAAGAGCCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 297
QY 241 TTCTCTCAAGATCAGCACTGTGACACCTGAGATCTCCACATCTACTGTCTCGAAG 300
DB 298 TTCTCTCAAGATCAGCACTGTGACACCTGAGATCTCCACATCTACTGTCTCGAAG 357
QY 301 GTCTCTCAAGTCCATGCTATGAGTACTAGGGGTCAGGAAACCTCAGTACAGCTCC 360
DB 358 GAGAT---TACGACGAGCTATGAGTACTAGGGGTCAGGAAACCTCAGTACAGCTCC 414
QY 361 TCA 363
DB 415 TCA 417

RESULT 9

US-08-436-463-1
Sequence 1, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-BODY AND GENE FRAGMENT CODING FOR SAID ANTI-BODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 21..449
US-08-436-463-1

Query Match 72.1%; Score 261.8; DB 1; Length 462;
Best Local Similarity 92.6%; Pred. No. 4.2e-81;
Matches 275; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 60
DB 78 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCACTCTG 137
QY 61 ACTTGTCTTCTCTGGGTTTTCAGTACACTTCTGTATGGGTGTGAGCTGGATTGCA 120
DB 138 ACTTGTCTTCTCTGGGTTTTCAGTACACTTCTGTATGGGTGTGAGCTGGATTGCGT 197
QY 121 CAGCCTTCAGGAAAGGCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAAAGCGC 180
DB 198 CAGCCTTCAGGAAAGGCTGAGTGGCTGGCAGACATTTGGTGGATGATGATTAATAC 257
QY 181 TATAACCATCCCTGAAGAGCCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 240
DB 258 TATAACCATCCCTGAAGAGCCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGGTA 317
QY 241 TTCTCTCAAGATCAGCACTGTGACACCTGAGATCTCCACATCTACTGTCTCGA 297
DB 318 TTCTCTCAAGATCAGCACTGTGACACCTGAGATCTCCACATCTACTGTCTCGA 374

RESULT 10
US-08-408-133-1
Sequence 1, Application US/08408133
Patent No. 5750078
GENERAL INFORMATION:
APPLICANT: SHITARA, Kenya
APPLICANT: HANAI, No. 5750078uo
APPLICANT: HASEGAWA, Mamoru
APPLICANT: MIYAJI, Hitomasa
APPLICANT: KUMANA, Yoshihisa
TITLE OF INVENTION: Process for Producing Humanized Chimera
TITLE OF INVENTION: Antibody
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: No. 5750078th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,133
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, Arthur R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (803)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: Hybridoma KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 256..262
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441..806
OTHER INFORMATION: /product- "RAT IMMUNOGLOBULIN HEAVY"
OTHER INFORMATION: CHAIN VARIABLE REGION
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 300..440
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 429..806)
OTHER INFORMATION:
US-08-408-133-1
Query Match 69.1%; Score 250.8; DB 1; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTAGTCTG 60
DB 441 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTAGTCTG 500
QY 61 ACTGTCTCTCTCTGCGTTTTCACGTAGCAGCTTCTGTATGGGTGTGAGCTGGATTGCA 120
DB 501 ACTGTCTCTCTCTGCGTTTTCACGTAGCAGCTTATGATGTGTGTGGGTGATGCTG 560
QY 121 CAGCCTTCAGGAAGGCTGTGGAGTGGCTGGCACATTTACTGGATGATGACAGCC 180
DB 561 CAGCTTCAGGAGGAGGCTGTGGAGTGGCTGGCAACGTTTGTGGAGTATGATGATGAC 620
QY 181 TATAACCATCCCGAAGAGCGGCTTACATCTCCAAAGTACTCCAGAACAGGTA 240
DB 621 TACATCCATCTCTGAAGAAACCGGCTCACATCTCCAAAGACCTCCAAACACCAAGCA 680
QY 241 TTCCTCAAGATCACAGTGTGACACATCGAGATCTGCACTACTGTCTCAAGG 300
DB 681 TTCCTCAAGATCACAGTGTGACACATCGAGATCTGCACTACTGTCTGCGGAGCA 740
QY 301 GTCTCTTACTGCTTATGCTA---TGCATCTAGGGGTCAAGAACCTCAGTCAGCTC 357
DB 741 GGGCTACGAGGAGGTATAGTGAAGCTTGTATGATGAGGGCCACGAGTCATGTCACAGTC 800
QY 358 TTCCTCA 363
DB 801 TTCCTCA 806
RESULT 11
US-08-454-683-1
Sequence 1, Application US/08454683
Patent No. 5807548
GENERAL INFORMATION:
APPLICANT: SHITARA, Kenya
APPLICANT: HANAI, No. 5807548uo
APPLICANT: HASEGAWA, Mamoru
APPLICANT: MIYAJI, Hitomasa
APPLICANT: KUMANA, Yoshihisa
TITLE OF INVENTION: Process for Producing Humanized Chimera
TITLE OF INVENTION: Antibody
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: No. 5807548th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,683
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/408,133
FILING DATE:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, Arthur R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (803)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE: N
STRAIN: Hybridoma KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 256..262
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441..806
OTHER INFORMATION: /product="RAT IMMUNOGLOBULIN HEAVY
OTHER INFORMATION: CHAIN VARIABLE REGION"
FEATURE:
NAME/KEY: s1g_peptide
LOCATION: 300..440
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 429..806)
OTHER INFORMATION:
US-08-454-683-1

Query Match 69.1%; Score 250.8; DB 1; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTGTGAAGAGCTGGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 60
DB 441 CAGGTTACTGTGAAGAGATCTGGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 500
QY 61 ACTTGTTCTTCTCTCTGGGTTTTCAGTGCAGCTTGTGGTATGGGTGTGAGCTGGATTGCA 120
DB 501 ACTTGTTCTTCTCTCTGGGTTTTCAGTGCAGCTTGTGGTATGGGTGTGAGCTGGATTGCA 560
QY 121 CAGCCTTCAGGAAGAGGTCTGGAGTGGCTGGCAGACATTTCAGTGGATGTGACAAAGCC 180
DB 561 CAGTCTTCAGGAAGAGGTCTGGAGTGGCTGGCAGAACTTTGGTGGATGTGCTAAAGTAC 620
QY 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGACCAAGCA 240
DB 621 TACAATCCATCTCTGAAAAACCGCTCAGATCTCCAGAGACCACTCCAAACCAAGCA 680
QY 241 TTCCCTCAAGATCACAGAGTGTGACACTCGAGATCTCCAGATCTACTGCTCGAAGG 300
DB 681 TTCCCTCAAGATCACCAATATGTGACACTCGAGATCTCCAGATCTACTGCTCGGAGGA 740
QY 301 GTCTCTACTACTGCTATGCTA---TGAGTACTGGGGTCAAGAACTTCAAGCTGACAGCTC 357
DB 741 GGGGCTACGAGAGGTATAGTACCTTTGATTACTGGGGCCAGGAGTCAATGTCTACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 12
US-08-116-778E-16
Sequence 16, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 261..267
US-08-116-778E-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTGTGAAGAGCTGGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 60
DB 441 CAGGTTACTGTGAAGAGATCTGGCCCTGGGATATTCGAGCCCTCCAGACCTTCAGTCTG 500
QY 61 ACTTGTTCTTCTCTCTGGGTTTTCAGTGCAGCTTGTGGTATGGGTGTGAGCTGGATTGCA 120
DB 501 ACTTGTTCTTCTCTCTGGGTTTTCAGTGCAGCTTGTGGTATGGGTGTGAGCTGGATTGCA 560
QY 121 CAGCCTTCAGGAAGAGGTCTGGAGTGGCTGGCAGACATTTCAGTGGATGTGACAAAGCC 180
DB 561 CAGTCTTCAGGAAGAGGTCTGGAGTGGCTGGCAGAACTTTGGTGGATGTGCTAAAGTAC 620
QY 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGAGATACCTCCAGACCAAGGA 240
DB 621 TACAATCCATCTCTGAAAAACCGCTCAGATCTCCAGAGACCACTCCAAACCAAGGA 680
QY 241 TTCCCTCAAGATCACAGAGTGTGACACTCGAGATCTCCAGATCTACTGCTCGAAGG 300
DB 681 TTCCCTCAAGATCACCAATATGTGACACTCGAGATCTCCAGATCTACTGCTCGGAGGA 740
QY 301 GTCTCTACTACTGCTATGCTA---TGAGTACTGGGGTCAAGAACTTCAAGCTGACAGCTC 357
DB 741 GGGGCTACGAGAGGTATAGTACCTTTGATTACTGGGGCCAGGAGTCAATGTCTACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 13
US-08-454-680-1

Sequence 1, Application US/08454680
Patent No. 5866692
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA
TITLE OF INVENTION: ANTIBODY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,680
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/408,133
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE: 17-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-238375
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 249-74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 256..262
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441..806
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 300..440
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 430..806)
US-08-454-680-1
Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
1 CAGGTTACTCTGAAGAAGATCTGGCCCTGGGATATTGCAGCCCTCCAGACCTCAGCTTG 60
|||||

Db 441 CAGGTTACTCTGAAGAAGATCTGGCCCTGGGATATTGCAGCCCTCCAGACCTCAGCTTG 500
QY 61 ACTGTTCTTCTCTCTGGGTTTTCAGTGACCACTTCTGATGAGGTGAGTGCATTCGA 120
|||||
Db 501 ACTTGCTCTTCTCTGGGTTTTCAGTGACCACTTGTGATGAGGTGAGTGCATTCGT 560
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGACACATTTACTGGAGATGACACACCG 180
|||||
Db 561 CAGCTTCAGGGAAGGGTCTGGAGTGGCTGGACACATTTACTGGAGATGACACACCG 620
QY 181 TATAACCCATCCCTGAAGAGCCGCTTACATCTCCAAAGATACCTCAGACCAAGTA 240
|||||
Db 621 TACAAATCCATCTCTGAAAAACCGCTCAAAATCTCCAAAGACACCTCAACAAACGA 680
QY 241 TTCCTCAAGATCAGACGATGGACATGAGATGATGACATGATGATGATGATGATG 300
|||||
Db 681 TTCCTCAAGATCAGACCAATATGACACCTGACATGATGATGATGATGATGATG 740
QY 301 GTCTCTTAACCTGCTTATGCTA--TGACACTAGTGGGTCAGGAACCTGACACCGTC 357
|||||
Db 741 GGGGCTACGAGAGGATAGTAGTGTGATTACTGAGGGCCAGGAGTATGATGATGATG 800
QY 358 TCCTCA 363
|||||
Db 801 TCCTCA 806
RESULT 14
US-08-438-562-16
Sequence 16, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

Tue Jul 15 10:45:08 2003

us-09-759-112a-5.ini

Page

MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 261..267
US-08-438-562-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAAGAGATCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTTCTTCTCTGGGTTTTCACGTAGACACTTCTGTATGGGTGTGAGCTGATTCGA 120
DB 501 ACTTGCTCTTCTCTGGGTTTTCACGTAGACACTTGTATGTGTGGGCTGATTCGT 560
QY 121 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCACATTTACTGGGATGATCAAGCC 180
DB 561 CAGTCTTCAGGAGGCTCTGAGTGGCTGGCAAAAGTTGGTGGAGTGTATCTAGTAC 620
QY 181 TATTAACCATCCCTGAAAGAGCCGCTTACAAATCTCCAGAGATACCTCCAGAACAGGTA 240
DB 621 TACAAATCATCTCTGAAAGAGCCGCTTACAAATCTCCAGAGACCTCCAGAACAGGTA 680
QY 241 TTCTCTAAGATCACCAGTGTGACACTCGAGATACCTGCCACATCTACTGTCTCGAAGG 300
DB 681 TTCTCTAAGATCACCAGATATGACACTCGAGATACCTGCCATATCTACTGTCTCGGAGA 740
QY 301 GTCTCTTAAGTCCCTATGCTA---TGGACTACTGGGGTGAAGAACCTCAGTACCCGTC 357
DB 741 GGGGCTACGAGGATATAGTGTGAGCTTGTATTACTGTGGGGCCAGGAGTCAATGTGCACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

RESULT 15
US-08-483-528B-16
Sequence 16, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUNAKI, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 261..267
US-08-483-528B-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;
Best Local Similarity 82.2%; Pred. No. 3.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAAGAGCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTGAAAGAGATCTGGCCCTGGGATATTGACAGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTTCTTCTCTGGGTTTTCACGTAGACACTTCTGTATGGGTGTGAGCTGATTCGA 120
DB 501 ACTTGCTCTTCTCTGGGTTTTCACGTAGACACTTGTATGTGTGGGCTGATTCGT 560
QY 121 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCACATTTACTGGGATGATCAAGCC 180
DB 561 CAGTCTTCAGGAGGCTCTGAGTGGCTGGCAAAAGTTGGTGGAGTGTATCTAGTAC 620
QY 181 TATTAACCATCCCTGAAAGAGCCGCTTACAAATCTCCAGAGATACCTCCAGAACAGGTA 240
DB 621 TTCTCTAAGATCACCAGTGTGACACTCGAGATACCTGCCATATCTACTGTCTCGAAGG 300
QY 241 TTCTCTAAGATCACCAGATATGACACTCGAGATACCTGCCATATCTACTGTCTCGGAGA 740
DB 681 TTCTCTAAGATCACCAGATATGACACTCGAGATACCTGCCATATCTACTGTCTCGGAGA 740
QY 301 GTCTCTTAAGTCCCTATGCTA---TGGACTACTGGGGTGAAGAACCTCAGTACCCGTC 357
DB 741 GGGGCTACGAGGATATAGTGTGAGCTTGTATTACTGTGGGGCCAGGAGTCAATGTGCACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

Search completed: July 10, 2003, 22:14:54
Job time : 54 secs

Tue Jul 15 10:45:09 2003

us-09-759-112a-5.rmpb

Page 1

GenCore Version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 22:13:44 : Search time 151 Seconds
(without alignments)
3795.863 Million cell updates/sec

Title: US-09-759-112A-5

Perfect score: 363
Sequence: 1 caggttactctgaagaagtc.....cctcagtcacgtctctctca 363

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications.NA.*

1: /cgn2.6/ptodata/2/pubpna/US07_NEM_PUB.seq.*
2: /cgn2.6/ptodata/2/pubpna/PCRT_NEM_PUB.seq.*
3: /cgn2.6/ptodata/2/pubpna/US06_NEM_PUB.seq.*
4: /cgn2.6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2.6/ptodata/2/pubpna/PCITUS_PUBCOMB.seq.*
6: /cgn2.6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
7: /cgn2.6/ptodata/2/pubpna/US08_NEM_PUB.seq.*
8: /cgn2.6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2.6/ptodata/2/pubpna/US09_NEM_PUB.seq.*
10: /cgn2.6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2.6/ptodata/2/pubpna/US10_NEM_PUB.seq.*
12: /cgn2.6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2.6/ptodata/2/pubpna/US60_NEM_PUB.seq.*
14: /cgn2.6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	100.0	363	US-09-759-112A-5	Sequence 5, Appl1
2	363	100.0	363	US-09-759-112A-6	Sequence 6, Appl1
3	313.4	86.3	483	US-09-879-461-3	Sequence 3, Appl1
4	311.8	85.9	423	US-09-879-461-9	Sequence 9, Appl1
5	299	82.4	369	US-09-995-529-11	Sequence 11, Appl1
6	284.4	78.3	465	US-09-881-823-7	Sequence 7, Appl1
7	250.8	69.1	812	US-10-195-752-16	Sequence 16, Appl1
8	250.8	69.1	812	US-10-265-713-1	Sequence 1, Appl1
9	250.8	69.1	812	US-09-764-304-1	Sequence 15, Appl1
10	179.2	49.4	288	US-09-995-529-15	Sequence 69, Appl1
11	178.6	49.2	684	US-09-972-656-69	Sequence 83, Appl1
12	172	47.4	684	US-09-972-656-83	Sequence 11, Appl1
13	171	47.1	423	US-09-879-461-11	Sequence 11, Appl1
14	168.4	46.4	646	US-09-736-457-1113	Sequence 1113, Appl1
15	168.4	46.4	646	US-09-902-941-1113	Sequence 1113, Appl1
16	168.4	46.4	646	US-09-849-526-1113	Sequence 1113, Appl1
17	168.4	46.4	646	US-10-017-754-1113	Sequence 1113, Appl1
18	165	45.5	714	US-08-940-544-4	Sequence 4, Appl1
19	163.2	45.0	378	US-09-740-002-15	Sequence 15, Appl1

20	163.2	45.0	1428	10	US-09-740-002-19	Sequence 19, Appl1
21	160.2	44.1	454	9	US-09-797-941A-1	Sequence 1, Appl1
22	158.8	43.7	378	10	US-09-740-002-13	Sequence 13, Appl1
23	158.8	43.7	1428	10	US-09-740-002-17	Sequence 17, Appl1
24	156.8	43.2	10517	9	US-10-059-261-1	Sequence 1, Appl1
25	156.6	43.1	5079	10	US-09-809-517A-41	Sequence 41, Appl1
26	156	43.0	750	10	US-10-730-374-1	Sequence 251, Appl1
27	153.8	42.4	369	9	US-10-207-655-251	Sequence 251, Appl1
28	152.8	42.1	1683	9	US-10-207-655-253	Sequence 253, Appl1
29	152.8	42.1	825	9	US-10-207-655-253	Sequence 36, Appl1
30	148.2	40.8	351	9	US-10-153-401-35	Sequence 3, Appl1
31	147.8	40.7	458	9	US-10-153-401-3	Sequence 3, Appl1
32	147.8	40.7	458	10	US-09-990-205-3	Sequence 65, Appl1
33	147.8	40.7	814	9	US-10-153-401-65	Sequence 7, Appl1
34	147.2	40.6	417	7	US-08-779-784-7	Sequence 7, Appl1
35	145.6	40.1	360	9	US-10-232-187-1	Sequence 3, Appl1
36	145.6	40.1	420	10	US-09-007-093-3	Sequence 36, Appl1
37	143.8	39.6	4145	9	US-10-001-934-36	Sequence 35, Appl1
38	143.8	39.6	5020	9	US-10-001-934-35	Sequence 37, Appl1
39	142.6	39.3	454	10	US-09-881-823-3	Sequence 34, Appl1
40	139.6	38.5	518	10	US-10-207-655-354	Sequence 35, Appl1
41	139.6	38.5	366	9	US-10-207-655-353	Sequence 35, Appl1
42	139.6	38.2	423	9	US-09-742-693-29	Sequence 356, Appl1
43	138.6	38.2	734	10	US-10-207-655-356	Sequence 357, Appl1
44	138.6	38.2	825	9	US-10-207-655-357	Sequence 357, Appl1
45	138.6	38.2	1536	9	US-10-207-655-357	Sequence 357, Appl1

ALIGNMENTS

RESULT 1
US-09-759-112A-5
Sequence 5, Application US/09759112A
Publication No. US20030100741A1
GENERAL INFORMATION:
APPLICANT: Mueller, Sybilie
TITLE OF INVENTION: KOHLER, Helmut
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTI
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759, 112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 363
TYPE: DNA
ORGANISM: mouse
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(362)
OTHER INFORMATION: 1F7 VH chain gene
US-09-759-112A-5
Query Match 100.0%; Score 363; DB 9; Length 363;
Best Local Similarity 100.0%; Pred. No. 9.7e-114;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CAGGTACTCTGAAGAAGTCTGCGCTTGCATATTCAGAGCCCTCCAGACCTCAGTCTG 60
|||||
1 CAGGTACTCTGAAGAAGTCTGCGCTTGCATATTCAGAGCCCTCCAGACCTCAGTCTG 60
61 ACTTCTCTCTCTGCTGCTTTCACATGACACTTGTGTAGGGGTGAGCTGATTCGA 120
|||||
61 ACTTCTCTCTCTGCTGCTTTCACATGACACTTGTGTAGGGGTGAGCTGATTCGA 120
121 CAGCTTCAGAAAGGCTCTGAGTGGCTGCGACACATTTACTGGATGATGACAAAGCC 180
|||||
121 CAGCTTCAGAAAGGCTCTGAGTGGCTGCGACACATTTACTGGATGATGACAAAGCC 180
181 TATACCCATCCCTGAAAGAGCGGCTTACATCTCCAGAGATACCTCCAGACACAGCTA 240
OY

Db	181	TATTAACCCATCCCTGAAAGACCGGCTTACAAATCTCCAAAGGATACCTCCAGCAACCCAGGTA	240
Qy	241	TTCCCTCAAGATCACCAAGTGTGGACACTGGAGATACTGCGACATACTACTGTGCTCCGAAG	300
Db	241	TTCCCTCAAGATCACCAAGTGTGGACACTGGAGATACTGCGACATACTACTGTGCTCCGAAG	300
Qy	301	GTCTCTCTAACTGCTATGCTATGGACTACTGGGGTCAAGGAACTCAAGTACACCGTCTCC	360
Db	301	GTCTCTCTAACTGCTATGCTATGGACTACTGGGGTCAAGGAACTCAAGTACACCGTCTCC	360
Qy	361	TCA	363
Db	361	TCA	363

```

RESULT 2
US-09-759-112A-6
: Sequence 6, Application US/09759112A
: Publication No. US20030100741A1
GENERAL INFORMATION:
APPLICANT: Mueller, Sybille
APPLICANT: Kohler, Heinz
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759, 112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
: LENGTH: 363
: TYPE: DNA
: ORGANISM: mouse
: FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(363)
OTHER INFORMATION: 1F7 VH chain gene
US-09-759-112A-6

```

Query Match	100.0%	Score 363	DB 9	Length 363
Best Local Similarity	100.0%	Pred. No. 9.7e-114		
Matches 363	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	CAGGTTACTCTGAAGAAGCTCTGGCCCTGGGATATTCAGCCCTCCACACCTCTAGTCTG	60	
Db	1	CAGGTTACTCTGAAGAAGCTCTGGCCCTGGGATATTCAGCCCTCCACACCTCTAGTCTG	60	
QY	61	ACTTGTCTTTTCTCTGGGTTTTCAGTGAACACTTCTGATGGGTGAGTGTGATTCGA	120	
Db	61	ACTTGTCTTTTCTCTGGGTTTTCAGTGAACACTTCTGATGGGTGAGTGTGATTCGA	120	
QY	121	CAGCCTTCAAGAAAGGTCGTGGAGTGGCTGGCACACATTCTCTGGGATGATGACAAGCGC	180	
Db	121	CAGCCTTCAAGAAAGGTCGTGGAGTGGCTGGCACACATTCTCTGGGATGATGACAAGCGC	180	
QY	181	TATAACCATCCCTGGAAGAGCCGGCTTCAATCTCCAAAGATATACCTCCAGCAACAGGTA	240	
Db	181	TATAACCATCCCTGGAAGAGCCGGCTTCAATCTCCAAAGATATACCTCCAGCAACAGGTA	240	
QY	241	TTCCGCAAGATCACCACAGTGTGGACACTGTGAGATCTCGCCACATCTACTGTGCTGGAAG	300	
Db	241	TTCCGCAAGATCACCACAGTGTGGACACTGTGAGATCTCGCCACATCTACTGTGCTGGAAG	300	
QY	301	GTCCTCTAATGCGCTATGCTATGAGTACTAGGGGGCTAAAGAACTCAGTCACGCTCC	360	
Db	301	GTCCTCTAATGCGCTATGCTATGAGTACTAGGGGGCTAAAGAACTCAGTCACGCTCC	360	
QY	361	TCA 363		
Db	361	TCA 363		

```

RESULT 3
US-09-879-461-3
; Sequence 3, Application US/09879461
; Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-Oct-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 64..483
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-879-461-3

Query Match 86.3%; Score 313.4; DB 9; Length 483;
Best Local Similarity 91.5%; Pred. No. 8; 8e-97;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

1 CAGGTACTCTGAAAGAGCTGGCCCTGGGATATGCAAGCCCTCCCAACCTCAGTTG 60
121 CAGGTACTCTGAAAGAGATCTGGCCCTGGGATATGCAAGCCCTCCCAACCTCAGTTG 180
61 ACTGTCTCTTCTCTGGGTTTTCACATGACACTCTGTATGGTGTGAGCTGATTCGA 120
181 ACTGTCTCTTCTCTGGGTTTTCACATGACACTCTGTATGGTGTGAGCTGATTCGT 240
121 CAGCCTTCAGAAAGAGGCTGAGAGTGGCTGGCACACATTACTGGAGATGACAAAGCC 180
241 CAGCCTTCAGAAAGAGGCTGAGAGTGGCTGGCACACATTACTGGAGATGACAAAGCC 300
181 TATTAACCCATCCTGAAAGAGCCGGCTTACATTCACAAGATACCTCAGCAACAGGTA 240
301 TATTAACCCATCCTGAAAGAGCCGGCTTACATTCACAAGATACCTCAGCAACAGGTA 360

```


1 CAGGTTTACCTCTGAAAAGAGCTCTGGGCCCCCTGGGAAATATTCACAGCCCCCAAGCCCCCAAGCTCTG 50

Db 181 TATAACCATCCCTGAAGAGCCGGCTCACAAATCTCCAAGGATACCTCCAGCAACCAGTA 240

241 TTCTCAGATCACCAGTGTGGACACTCGAGATCTACTGCCACATCTACTGTGCTGAAGG 300

Db 241 TTCCTAAGATACCACTGTGGACACTGACAGATACCTCCACTACTACTGTCTCGAGA 300
Qy 301 G-----TCTCTTAAGTCCCTATGCTATGAGTACTGGGTCAAGAACCTCAGTACC 354
Db 301 GCTAAGTATGTTAAACCCCTACTATGCTATGAGTACTGGGTCAAGAACCTCAGTACC 360
Qy 355 GTCTCTCA 363
Db 361 GTCTCTCA 369

RESULT 6

US-09-881-823-7
; Sequence 7, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(441)
US-09-881-823-7

Query Match 78.3%; Score 284.4; DB 10; Length 465;
Best Local Similarity 88.0%; Pred. No. 6,8e-87;
Matches 322; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 1 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACGCCCTCCAGACCTCAGTCTG 60
Db 70 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACGCCCTCCAGACCTCAGTCTG 129
Qy 61 ACTTGTCTTCTCTGGGTTTTCAGTACGACTTCTGTATGGGTGAGCTGATTCGA 120
Db 130 ACTTGTCTTCTCTGGGTTTTCAGTACGACTTGTATGGGATGAGGCTGATTCGT 189
Qy 121 CAGCCTTCAGAAAGGCTGTGAGTGGCTGGACACATTTACTGGATGAGCAAGCGC 180
Db 190 CAGCCTTCAGAGGAGGTCTGAGTGGCTGGACACATTTGTTGGAATGATTAAGTAC 249
Qy 181 TATAACCATCCCTGAAGACCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
Db 250 TATAACCATCCCTGAAGACCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 309
Qy 241 TTCTCTCAAGTACAGTGTGACACTCGAGATCTCCCATACTACTGTCTCGAAG 300
Db 310 TTCTCTCAAGTACAGTGTGACACTCGAGATCTCCCATACTACTGTCTCGAATA 369
Qy 301 GTCTCTCAAGTACAGTGTGACACTCGAGATCTCCCATACTACTGTCTCGAAG 357
Db 370 GAGGGGGCTGGGGCTACGATGTATGACTACTGGGGTCAAGAACTCTGATCACCCTC 429
Qy 358 TCCTCA 363
Db 430 TCCTCA 435

RESULT 7

US-10-195-752-16
; Sequence 16, Application US/10195752
; Publication No. US20030077276A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU

TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/195,752

FILING DATE: 16-Jul-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/393,385B

FILING DATE: 27-JUN-96

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)816-4000

TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 812 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

STRAIN: HYBRIDOMA KM50

FEATURE:

NAME/KEY: TATA_signal

LOCATION: 261..267

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-195-752-16

Query Match 69.1%; Score 250.8; DB 9; Length 812;
Best Local Similarity 82.2%; Pred. No. 2.3e-75;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

Qy 1 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACGCCCTCCAGACCTCAGTCTG 60
Db 441 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATGACGCCCTCCAGACCTCAGTCTG 500
Qy 61 ACTTGTCTTCTCTGGGTTTTCAGTACGACTTCTGTATGGGTGAGCTGATTCGA 120
Db 501 ACTTGTCTTCTCTGGGTTTTCAGTACGACTTGTATGGGATGAGGCTGATTCGT 560
Qy 121 CAGCCTTCAGAAAGGCTGTGAGTGGCTGGACACATTTACTGGATGAGCAAGCGC 180
Db 561 CAGCCTTCAGAGGAGGTCTGAGTGGCTGGACACATTTGTTGGAATGATTAAGTAC 620
Qy 181 TATAACCATCCCTGAAGACCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 240
Db 621 TATAACCATCCCTGAAGACCGCGCTTACAATCTCCAAGATACCTCCAGCAACAGTA 680
Qy 241 TTCTCTCAAGTACAGTGTGACACTCGAGATCTCCCATACTACTGTCTCGAAG 300
Db 681 TTCTCTCAAGTACAGTGTGACACTCGAGATCTCCCATACTACTGTCTCGAAGA 740

61 ACTTGTCTTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTTCGA 120

0
0
0
0
0
0
0

Query Match 69.18; Score 250.8; DB 10; Length 812;

Best Local Similarity 82.28; Pred. No. 2.3e-75;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1

QY	CAGGTTACGCTGAAGAGAGTCGGCCCTGGGAAATATGGACGCCCTCCAGACCCCTCAGTCG	60
Db	441 CAGGTTACTCTGAAAGAAATCTGGCCCTGGGATATGGACGCCCTCCAGACCCCTCAGTCG	5000
QY	61 ACTTGTCTCTTCCTGGGTTTTCACTGAGCACTTCCTGGTATGGGTGGAGCTGGATTGGA	120
Db	501 ACTTGTCTCTTCCTGGGTTTTCACTGAGCACTTATGTGTATGTGTGGGTGGATTGCT	5600
QY	121 CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTCTGGGATGATGACACGCC	180
Db	561 CAGCTCTTCAGGGAAAGGGTCTGGAGTGGCTGGCAACGTTTGGTGGAGTGAATGCTAAATAC	620
QY	181 TATTAACCCATCCCTGGAAGAGCCGGCTTTCATCTCCAGATGACTCAGCAATCCAGTA	240
Db	621 TACAAATCCATCTCTGAAAAACCGGCTCACAAATCTTCCAAAGGACACCTCCAAACAAAGCA	680
QY	241 TTCCTCAAGATCACCCAGTGTGGACACTCGAGATACTGCCACATCTACTGTGTCGAAGG	300
Db	681 TTCCTCAAGATCACCAATATGGACACTCGAGATCTGCGATATACTACTGTGCTGGGAGA	740
QY	301 GTTCTCTTAATGCTCCTATGCTA---TGGACTACTGTGGGTCAAGGAACTCAGTACCCGTC	357
Db	741 GGGGCTACGAGAGGATATAGTGAAGCTTTGATTACTGTGGGCCACGAGATCATGTGTACAGTC	8000
QY	358 TCCTCA 363	
Db	801 TCCTCA 806	

RESULT 10
US-09-995

Sequence 15, Application US/09955529
Publication No. US2003009655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
FILE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 288
TYPE: DNA
ORGANISM: Homo sapiens
US-09-995-529-15

Query Match	49.48;	Score 179.2;	DB 9;	Length 288;
Best Local Similarity	76.48;	Pred. No. 4.3e-51;		
Matches 220; Conservative	0;	Mismatches 68;	Indels 0;	Gaps 0;

OY	1	CAGGTACTCTTAAAGAGCTGCGCCCTGGGATTTTGGACGCCCTCCAGACCCCTCAGCTG	60
Db	1	CAGGTACTCTTAAAGAGCTGCTGCTCTCGCTGGTGAATCCACACAGACCTTCACACTG	60
OY	61	ACTTGTCTTCTCTCTGGGTTTTCACGTAGCACTTCTGGTATGGGTGTAGACTGGATTCGA	120
Db	61	ACTGTGACCTTCTCTGGGTTTTCACGTAGCACTATGGTAAATGGCTGTAGACTGGATTCG	120
OY	121	CAGCCTTCAGGAAAGGCTGTGAGTGTGCTGGCAGACATTTACTGGATGATGACAAAGCGC	180
Db	121	CAGCCTTCAGGAAAGGCTGTGAGTGTGCTGGCAGCATTGATTTGGATGTGATTAATTC	180
OY	181	TATTAACCATCCCTGAAAGCGCGGTTTCATATCTCCAAAGATTAACCTCAGACCAACAGTA	240
Db	181	TACAGCACATCTCTGAAGCAGAGCTCCACATCTCCAAAGACACCTCCAAAACACAGGTG	240

Qy 241 TTCCTCAAGATCACCAGAGTGTGGACACTCGAGATACTCTGCCACATACTAC 288
||| | | ||| |||| | | | | |||| | |||
Db 241 GTCCCTACAAATGACCAACATGGAGCCCTGTGGACACAGCCACGATATTAC 288

RESULT 11
US-09-972

```

? Sequence 69, Application US/09972656
? Publication No. US20030099647A1
? GENERAL INFORMATION:
? APPLICANT: Deshpande, Rajendra
? APPLICANT: Teal, Mel-Mel
? TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
? TITLE OF INVENTION: Neutralizing Activity
? FILE REFERENCE: A-799
? CURRENT APPLICATION NUMBER: US/09/972,656
? CURRENT FILING DATE: 2001-10-05
? NUMBER OF SEQ ID NOS: 135
? SOFTWARE: Patentin version 3.0
? SEQ ID NO 69
? LENGTH: 666
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(666)
? US-09-972-656--69

```

Query Match	49.28;	Score 178.6;	DB 9;	Length 666;
Best Local Similarity	70.88;	Pred. No. 9.2e-51;		
Matches 254; Conservative	0;	Mismatches 99;	Indels 6;	Gaps 1

[illegible]

RESULT 12
US-09-972

```

: Sequence 83:Application US/09972656
: Publication No.: US20030099647A1
: GENERAL INFORMATION:
: APPLICANT: Deshpande, Rajendra
: APPLICANT: Tsai, Mei-Mei
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: TITLE OF INVENTION: Neutralizing Activity
: FILE REFERENCE: A-799
: CURRENT APPLICATION NUMBER: US/09/972,656
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ. ID NOS: 135
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 83
: LENGTH: 684

```

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(684)
US-09-972-656-83

Query Match 47.4%; Score 172; DB 9; Length 684;
Best Local Similarity 69.4%; Pred. No. 1.7e-48;
Matches 254; Conservative 0; Mismatches 100; Indels 12; Gaps 1;

QY 6 TACTCTGAAGAGTCTGGCCCTGGAGATATGACACCCCTCCAGACCCCTCACTGACTTG 65
DB 6 TACCTTGAGAGAGTCTGCTCTACGCTGCTGCAACCCGACAGACCCCTCAGCTGACCTG 65
QY 66 TTTCTTCTCTGGGTTTTCACGACACTCTGTGTATGGGTGTGAGCTGAGATTCAGACGCC 125
DB 66 CTCTCTACTCTGGGTCTCTACACAGTAATGAAGCGGGTGTGGCTGGATCCCTCAAGCC 125
QY 126 TTCAGAAAGGCTGTGGAGTGGTGCACACATTTACTGGAGTATGACAGCGCTATTA 185
DB 126 CCCAGGAAAGGCCCGGAGTGGCTTGCATCTTTATGGATGATATAGCCGCTACAG 185
QY 186 CCCATCCCTGAAGACCGGCTTACATCTCCAGAGATACCTCCAGCAACGAGTATTCCT 245
DB 186 CCCCTCTGTGAGAGCAGGCTCATCGTTAACAGAGACCTCCAAAGCCAGGTTGCT 245
QY 246 CAATATCACAGTGTGACACTCGAGATACCTCCACATACACTGTGCTGCAAGGTTTC 305
DB 246 TACATATGACCAATGACACCTGTGACACGCGCAATATTAATGTGACACAGACTGCT 305
QY 306 TCTACTG-----CCTATGCTATGACTACTGAGGTCAGAGAACCTCAGTAC 353
DB 306 CAGATATGCTGCTACTCAACGCGGTGTTTGTATGATGTCTGGGGCCAGAGGACAGGTCAC 365
QY 354 CGTCTC 359
DB 366 CGTCTC 371

RESULT 13
US-09-879-461-11
Sequence 11, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-879-461-11

Query Match 47.1%; Score 171; DB 9; Length 423;
Best Local Similarity 66.9%; Pred. No. 3.1e-48;
Matches 243; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGAGATATGACACCCCTCCAGACCCCTCACTG 60
DB 61 CAGGTACTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 61 ACTGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 121 ACTGCACTCTCTCGGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 121 CAGCTTCAGAAAGGCTGTGAGTGGTGCACACATTTACTGGAGTATGACAGAGCC 180
DB 181 CAGCCCGCGGTAAAGCTGTAAGTGGTGCCTACATCTAGTGGAGAGACAAAGT 240
QY 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCAAGATACCTCCAGCAACAGGTA 240
DB 241 TACAACCGAGCCCGAATATCCGCTGTGACGATATCCAAAGACCTCCGTAACAGGTT 300
QY 241 TTCCTCAAGATCACAGTGTGACACTCGAGATACCTGCAATACCTACTGTGTGGAAG 300
DB 301 GTTCTGACATGACTATCATGACCGCGTTGACACCGCTACTACTGTGCTGACGC 360
QY 301 GTCCTCTAAGTGCCTATGATGAGTACGACGAGGAGTCAAGAACTGACACGCTGCC 360
DB 361 GAACCGTTTCTACTGCTACTGACTGACGTTTGGGTCGTGGTACCCAGTTACCGTAGC 420
QY 361 TCA 363
DB 421 TCA 423

RESULT 14
US-09-736-457-1113
Sequence 1113, Application US/09736457
Patent No. US20020168637A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Derrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1113
LENGTH: 646
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(646)
OTHER INFORMATION: n = A,T,C or G
US-09-736-457-1113

Query Match
Best Local Similarity 46.4%; Score 168.4; DB 9; Length 646;
Matches 257; Conservative 0; Mismatches 106; Indels 15; Gaps 1;
Pred. No. 2.7e-47;

1 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATTCAGAGCCCTCCAGACCCCTCAGTCTG 60
65 CAGGTACCTTGAAGAGTGTGGCTGTCTGTACTGTGTAAACCAAGAGACCTCCAGCCTG 124
61 ACTTGTCTTCTCTGGGTTTTCAGTACGACCTTGTGTAGGTGGTGTGAGCTGATTCGA 120
125 ACCTGCACCGTCTCTGGGTTTTCAGTACGATATTTAGAGTGGGTGTGAGTGGATCCGT 184
121 CAGCTTCAAGAAAGGCTGTGAGTGGCTGGCACACATTTACTGGATGATGACACAGCG 180
185 CAGCCCCCAGGAAAGGCGCTGTGAGTGGTTGCATACATTTTTCGACTGACGAAAAATCC 244
181 TATTAACCATCCCTGAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACCAAGTA 240
245 TTCAATTCATCTCTGAAGAAAGGCTGTACCATCTCCAGAGACCTTAAAGCCAGGTG 304
241 TTCCCTCAAGATCAACAGTGTGACACTGAGATACCTGACATACCTACTGTGCTG---- 296
305 GTCTTAGCATGACCAACATGAGACCTGTGAGACACACCAATATTTCTGTGACGGCTC 364
297 -----AAGGCTCTCTTACTGCTTATGCTATGCTAGTACACTACTGAGGCTCAAGAAC 345
365 TCTATTTACTCTGGGGGATTAGAAACCTACCAATACATGACGCTGTGGGCAAGGGACC 424
346 TCAGTACCGCTCTCCCTCA 363
425 ACCGCCACCGCTCTCTCA 442

RESULT 15

US-09-902-941-1113
Sequence 1113, Application US/09902941
Patient No. US20020172952A1

GENERAL INFORMATION:

APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tonglong
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Warnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
NUMBER OF SEQ ID NOS: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1113
LENGTH: 646
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc_feature
LOCATION: 529, 580, 622
OTHER INFORMATION: n = A,T,C or G
US-09-902-941-1113

Query Match
Best Local Similarity 46.4%; Score 168.4; DB 9; Length 646;
Matches 257; Conservative 0; Mismatches 106; Indels 15; Gaps 1;
Pred. No. 2.7e-47;

1 CAGGTACTCTGAAAGAGTGTGGCCCTGGGATATTCAGAGCCCTCCAGACCCCTCAGTCTG 60
65 CAGGTACCTTGAAGAGTGTGGCTGTCTGTACTGTGTAAACCAAGAGACCTCCAGCCTG 124
61 ACTTGTCTTCTCTGGGTTTTCAGTACGACCTTGTGTAGGTGGTGTGAGCTGATTCGA 120
125 ACCTGCACCGTCTCTGGGTTTTCAGTACGATATTTAGAGTGGGTGTGAGTGGATCCGT 184
121 CAGCTTCAAGAAAGGCTGTGAGTGGCTGGCACACATTTACTGGATGATGACACAGCG 180
185 CAGCCCCCAGGAAAGGCGCTGTGAGTGGTTGCATACATTTTTCGACTGACGAAAAATCC 244
181 TATTAACCATCCCTGAAGAGCGGCTTACAATCTCCAAGATACCTCCAGCAACCAAGTA 240
245 TTCAATTCATCTCTGAAGAAAGGCTGTACCATCTCCAGAGACCTTAAAGCCAGGTG 304
241 TTCCCTCAAGATCAACAGTGTGACACTGAGATACCTGACATACCTACTGTGCTG---- 296
305 GTCTTAGCATGACCAACATGAGACCTGTGAGACACACCAATATTTCTGTGACGGCTC 364
297 -----AAGGCTCTCTTACTGCTTATGCTATGCTAGTACACTACTGAGGCTCAAGAAC 345
365 TCTATTTACTCTGGGGGATTAGAAACCTACCAATACATGACGCTGTGGGCAAGGGACC 424
346 TCAGTACCGCTCTCCCTCA 363
425 ACCGCCACCGCTCTCTCA 442

Search completed: July 10, 2003, 22:17:40
Job time: 154 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2003, 22:13:44 ; Search time 1741 Seconds
(without alignments)
3376.773 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363

Sequence: 1 caggttactctgaagagtc.....ccctcagtcacgtctctca 363

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: *

- 1: em_estdb:*
- 2: em_estdb:*
- 3: em_estdb:*
- 4: em_estdb:*
- 5: em_estdb:*
- 6: em_estdb:*
- 7: em_estdb:*
- 8: em_estdb:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_est3:*
- 12: gb_est4:*
- 13: gb_est5:*
- 14: gb_est6:*
- 15: em_estfun:*
- 16: em_estfun:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rdg:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302.6	83.4	864	10	BE309336 601093720
2	300.6	82.8	913	12	BF583109 602098016
3	298.6	82.3	666	13	BG963642 602828443
4	295.8	81.3	940	12	BF178694 601806679
5	292.6	80.6	947	14	BQ943210 AGENCCOURT
6	281.4	77.5	652	13	BG963304 602827722

7	278	76.6	391	10	AW989547
8	271.6	74.8	920	14	BQ231128
9	267.6	73.7	379	10	BB872138
10	262.6	72.3	363	10	BB870162
11	262.4	72.3	366	10	BB870127
12	260.6	71.8	438	9	AA880491
13	259.8	71.6	900	12	BF581194
14	259.6	71.5	377	10	BB873796
15	259.6	71.5	589	17	A2882936
16	254.2	70.0	920	12	BF580719
17	253.4	69.8	920	10	BE289865
18	243.6	67.1	374	10	BB868022
19	237	65.3	769	12	BF582574
20	234.8	64.7	340	10	BB869851
21	224	61.7	330	10	BB870527
22	207.8	57.2	827	12	BM007964
23	206.2	56.8	904	12	BG758540
24	200.6	55.3	311	9	A1466485
25	196.6	54.2	945	14	BQ708104
26	196.6	54.2	945	14	BQ708104
27	195	53.7	1083	13	B1762661
28	191.8	52.8	384	10	BE246586
29	191.8	52.8	385	10	BE247351
30	191.6	52.8	923	12	BF663900
31	190.2	52.4	439	10	BE247437
32	189	52.1	955	14	BQ711772
33	189	52.1	955	14	BQ709744
34	188.2	51.8	324	10	BB872886
35	186.8	51.5	620	14	BM788928
36	186.8	51.5	620	14	BM788928
37	186.2	51.3	953	14	BQ709902
38	183.2	50.5	432	10	AW630601
39	181	49.9	783	12	BG340576
40	180.6	49.8	924	12	BG756803
41	179.6	49.5	931	12	BF663492
42	179	49.3	955	14	BQ878660
43	177.8	49.0	674	14	BM691116
44	176.6	48.7	761	13	BM008301
45	176.6	48.7	801	13	BM008059

ALIGNMENTS

RESULT 1
LOCUS BE309336 864 bp mRNA linear EST 26-OCT-2000
DEFINITION 601093720F1 NCI CGAP Mams Mus musculus CDNA clone IMAGE:3488309 5',
ACCESSION BE309336
VERSION BE309336.1 GI:9167366
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs@mail.nih.gov

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNI at:
http://image.llnl.gov
Plate: LAM8527 row: h column: 06
High quality sequence stop: 645.
Location/Qualifiers
1. .864

FEATURES
source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:348309"
/clone_1lb="NCI CGAP Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lotmar Hennighausen/Robin Humphreys, NIH"
BASE COUNT 171 a 260 c 222 g 211 t
ORIGIN

Query Match 83.4%; Score 302.6; DB 10; Length 864;
Best Local Similarity 92.2%; Pred. No. 1.3e-82;
Matches 344; Conservative 0; Mismatches 19; Indels 10; Gaps 2;

1 CAGGTACTCTGAAAGAGTCTGCGCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
43 CAGGTACTCTGAAAGAGTCTGCGCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 102
61 ACTGTTTCTTCTCTGGGTTTCTCAGTACGACCTCTGTGTGTGTGTGTGTGTGTGTG 119
103 ACTGTTTCTTCTCTGGGTTTCTCAGTACGACCTCTGTGTGTGTGTGTGTGTGTGTG 162
120 ACAGCCTTCAGAAAGGCTGTGGAGTGGCGACACATTTACTGGGATGATACAAAGC 179
163 TCAGCCTTCAGAAAGGCTGTGGAGTGGCGACACATTTACTGGGATGATACAAAGC 222
180 CTATTAACCATCCCTGAAAGAGCGGCTTACAAATCTCCAAAGATACCTCCAGCAAGGT 239
223 CTATTAACCATCCCTGAAAGAGCGGCTTACAAATCTCCAAAGATACCTCCAGCAAGGT 282
240 ATTCTCTAGAGTACACAGTGTGACACTGAGATCTGCCAATCTACTGTCTGTGAAG 299
283 ATTCTCTAGAGTACACAGTGTGACACTGAGATCTGCCAATCTACTGTCTGTGAAG 342
300 GGTCTCTCTACTG-----CTATGCTATGACTACTGGGGTCAAGAACCTCAGT 350
343 TTATTTACACAGGTGAGCTTACTTATGCTATGACTACTGGGGTCAAGAACCTCAGT 402
DB 351 CACCGTCTCTCTCA 363
QY 403 CACCGTCTCTCTCA 415

RESULT 2 583109 913 bp mRNA linear EST 12-DEC-2000
LOCUS BF583109 602098016F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4218099 5',
DEFINITION mRNA sequence.
ACCESSION BF583109
VERSION BF583109.1 GI:11656827
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 913)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

http://image.lnl.gov
Plate: LIAM9797 row: p column: 04
High quality sequence stop: 656.
Location/Qualifiers
1. 913
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4218099"
/clone_1lb="NCI CGAP Co24"
/lab_host="DH10B (r1 phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 183 a 261 c 250 g 219 t
ORIGIN

Query Match 82.8%; Score 300.6; DB 12; Length 913;
Best Local Similarity 90.5%; Pred. No. 5.5e-82;
Matches 334; Conservative 0; Mismatches 29; Indels 6; Gaps 1;

1 CAGGTACTCTGAAAGAGTCTGCGCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 60
60 CAGGTACTCTGAAAGAGTCTGCGCTGGGATATTCAGCCCTCCAGACCTCAGTCTG 119
61 ACTGTTTCTTCTCTGGGTTTCTCAGTACGACCTCTGTGTGTGTGTGTGTGTGTGTG 120
120 ACTGTTTCTTCTCTGGGTTTCTCAGTACGACCTCTGTGTGTGTGTGTGTGTGTGTG 179
121 CAGCCTTCAGAAAGGCTGTGGAGTGGCGACACATTTACTGGGATGATACAAAGC 180
180 CAGCCTTCAGAAAGGCTGTGGAGTGGCGACACATTTACTGGGATGATACAAAGC 239
181 TATTAACCATCCCTGAAAGAGCGGCTTACAAATCTCCAAAGATACCTCCAGCAAGGT 240
240 TATTAACCATCCCTGAAAGAGCGGCTTACAAATCTCCAAAGATACCTCCAGCAAGGT 299
241 TTCTCTAAGTACACAGTGTGACACTGAGATCTGCCAATCTACTGTCTGTGCTG--- 296
300 TTCTCTAAGTACACAGTGTGACACTGAGATCTGCCAATCTACTGTCTGTGCTGCTG 359
297 --AAGGCTCTCTTAACTGCTTATGCTATGAGTACTGGGGTCAAGAACCTCAGTACC 354
360 TATGATGCTTACCATATTTACTATGCTGTGACTGAGTGGGGTCAAGAACCTCAGTACC 419
DB 355 GTCTCTCTCA 363
QY 420 GTCTCTCTCA 428

RESULT 3 BG963642 666 bp mRNA linear EST 12-JUN-2001
LOCUS BG963642 602828443F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983155 5',
DEFINITION mRNA sequence.
ACCESSION BG963642
VERSION BG963642.1 GI:14351279
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 666)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

20

FEATURES

BASE COUNT

ORIGIN

Query Mat Best Loca

Matches

QY

Db

QY

DB

20

DB

2007

DB

2 0

DB

by

225

uy
ph

22

RESULT 5
PO943210

BY 343210
LOCUS
DEFINITION

DEFINITION
ACCESSION

ACCESSION
VERSION
REVIEWS

KEYWORDS
SOURCE
ORGANISM

WCTN13M

REFERENCE

EXHIBIT TITLE

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM13896 row: 0 column: 20
High quality sequence stop: 669.
Location/Qualifiers
1. 947
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="6398059"
/clone_id="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

BASE COUNT 218 a 272 c 235 g 221 t 1 others
ORIGIN
Query Match 80.6%; Score 292.6; DB 14; Length 947;
Best Local Similarity 87.9%; Pred. No. 1.7e-79;
Matches 319; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 60
DB 72 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 131
OY 61 ACTGTCT 120
DB 132 ACTGTCT 191
OY 121 CAGCCTTCAGGAAAGAGTCTGGAGTGGCTGGACACATTTACTGGATGATGACAAAGCCG 180
DB 192 CAGCCTTCAGGAAAGAGTCTGGAGTGGCTGGACACATTTACTGGATGATGACAAAGCCG 251
OY 181 TATTAACCATCCCTGAAAGAGCCGCTTACATCTCCAGAGATACCTCCAGCAACAGGTA 240
DB 252 TATTAACCATCCCTGAAAGAGCCGCTTACATCTCCAGAGATACCTCCAGCAACAGGTA 311
OY 241 TTCTCTCAAGATCCAGATGAGACACTGAGATATCTCCATCTACTGTCTCGAAG 300
DB 312 TTCTCTCAAGATCCAGATGAGACACTGAGATATCTCCATCTACTGTCTCGAATA 371
OY 301 GTCTCTCACTGCTTATGATGACTACTGAGGATCAAGAACTTCACTGCTCGTCC 360
DB 372 AGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 431
OY 361 TCA 363
DB 432 TCA 434

RESULT 6
LOCUS BG963304 652 bp mRNA linear EST 12-JUN-2001
DEFINITION 602827722F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982549 5',
mRNA sequence.
ACCESSION BG963304
VERSION BG963304.1 GI:14350941
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 652)
Mammalia: Eutheria, Rodentia, Sclurognathu: Muridae; Murinae; Mus.

AUTHORS
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10985 row: 1 column: 06
High quality sequence stop: 648.
Location/Qualifiers
1. 652
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="4982549"
/clone_id="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

BASE COUNT 141 a 184 c 163 g 164 t
ORIGIN
Query Match 77.5%; Score 281.4; DB 13; Length 652;
Best Local Similarity 86.0%; Pred. No. 4.2e-76;
Matches 312; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

OY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 60
DB 53 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCTCAGTCTG 112
OY 61 ACTGTCT 120
DB 113 ACTGTCT 172
OY 121 CAGCCTTCAGGAAAGAGTCTGGAGTGGCTGGACACATTTACTGGATGATGACAAAGCCG 180
DB 173 CAGCCTTCAGGAAAGAGTCTGGAGTGGCTGGACACATTTACTGGATGATGACAAAGCCG 232
OY 181 TATTAACCATCCCTGAAAGAGCCGCTTACATCTCCAGAGATACCTCCAGCAACAGGTA 240
DB 233 TATTAACCATCCCTGAAAGAGCCGCTTACATCTCCAGAGATACCTCCAGCAACAGGTA 292
OY 241 TTCTCTCAAGATCCAGATGAGACACTGAGATATCTCCATCTACTGTCTCGAAG 300
DB 293 TTCTCTCAAGATCCAGATGAGACACTGAGATATCTCCATCTACTGTCTCGATTG 352
OY 301 GTCTCTCACTGCTTATGATGACTACTGAGGATCAAGAACTTCACTGCTCGTCC 360
DB 353 CCTTATTTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 412
OY 361 TCA 363
DB 413 TCA 415

RESULT 7
LOCUS AW989547 391 bp mRNA linear EST 02-JUN-2000
DEFINITION u91406.v1 Soares_mammary_gland_NLMG Mus musculus cDNA clone
IMAGE:1531643 5' similar to SW:HVZH.HUMAN P04438 IG HEAVY CHAIN
V-JI REGION SESS PRECURSOR. [1]; mRNA sequence.
ACCESSION AW989547
VERSION AW989547.1 GI:8184975
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 391)
 NCI-CCAP <http://www.nci.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 TITLE Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
 MG1:947743
 Trace considered overall poor quality
 Seq primer: -40RP from Glibco
 High quality sequence stop: 1.

FEATURES

Source

1. 391
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:1531643"
 /clone_lib="Soares_mammary_gland_MMLMG"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Benito Soares and M. Fatima Bonaldo."

BASE COUNT

88 a 107 c 90 g 106 t

ORIGIN

Query Match 76.6%; Score 278; DB 10; Length 391;
 Best Local Similarity 95.0%; Pred. No. 3.9e-75;
 Matches 287; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 CAGGTACTCGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCACTGTG 60
 |||||||
 DB 56 CAGGTACTCGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCACTGTG 115
 |||||||
 QY 61 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGATGGAGTGGATGCA 120
 |||||||
 DB 116 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGATGGAGTGGATGCA 175
 |||||||
 QY 121 CAGCCTTCAGGAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCGC 180
 |||||||
 DB 176 TAGCCTTCAGGAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCGT 235
 |||||||
 QY 181 TATTAACCATCCCTGGAAGAGCCGGCTTACATCTCCAGAGATPACCTCCAGACAGGTA 240
 |||||||
 DB 236 TATTAACCATCCCTGGAAGAGCCGGCTTACATCTCCAGAGATPACCTCCAGACAGGTA 295
 |||||||
 QY 241 TTCTCAAGATCACCAGTGTGGACATCGATACATCTACTGATGCTGGAAG 300
 |||||||
 DB 296 TTCTCAAGATCACCAGTGTGGACATCGATACATCTACTGATGCTGGAAG 355
 |||||||
 QY 301 GT 302
 ||
 DB 356 GT 357

RESULT 8
 BQ231128 920 bp mRNA linear EST 02-MAY-2002
 LOCUS AGENCOURT.7578094 NCI CGAP.St1 Mus musculus cDNA clone
 DEFINITION IMAGE:6051673 5', mRNA sequence.
 ACCESSION BQ231128
 VERSION BQ231128.1 GI:20412528
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 920)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LHAM1305 row: 0 column: 02
 High quality sequence stop: 640.

FEATURES

Source

1. 920
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:6051673"
 /clone_lib="NCI CGAP.St1"
 /lab_host="DH10B (TL-resistant)"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.77 kb. Library constructed by Life Technologies. Note: this is a NCI/CGAP library."

BASE COUNT

205 a 264 c 224 g 222 t

ORIGIN

Query Match 74.8%; Score 271.6; DB 14; Length 920;
 Best Local Similarity 85.8%; Pred. No. 5.1e-73;
 Matches 314; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 CAGGTACTCGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCACTGTG 60
 |||||||
 DB 31 CAGGTACTCGAAGAAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCTCACTGTG 90
 |||||||
 QY 61 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGATGGAGTGGATGCA 120
 |||||||
 DB 91 ACTGTCTCTCTCTGGGTTTCACTGAGCACTTCTGGTATGGGATGGAGTGGATGCA 150
 |||||||
 QY 121 CAGCCTTCAGGAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCGC 180
 |||||||
 DB 151 CAGCCTTCAGGAAGGCTCTGAGTGGCTGGCACACATTTACTGGATGATGACAGCGC 210
 |||||||
 QY 181 TATTAACCATCCCTGGAAGAGCCGGCTTACATCTCCAGAGATPACCTCCAGACAGGTA 240
 |||||||
 DB 211 TATTAACCATCCCTGGAAGAGCCGGCTTACATCTCCAGAGATPACCTCCAGACAGGTA 270
 |||||||
 QY 241 TTCTCAAGATCACCAGTGTGGACATCGATACATCTACTGATGCTGCA 297
 |||||||
 DB 271 TTCTCAAGATCACCAGTGTGGACATCGATACATCTACTGATGCTGCA 330
 |||||||
 QY 298 AGGCTCTCTCACTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 357
 |||||||
 DB 331 AGGCTCTCTCACTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 390
 |||||||
 QY 358 TCCTCA 363
 |||||||
 DB 391 TCCTCA 396

RESULT 9
 BB872138 379 bp mRNA linear EST 27-NOV-2001
 LOCUS BB872138
 DEFINITION BB872138 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630034P22 5', mRNA sequence.
 ACCESSION BB872138
 VERSION BB872138.1 GI:17118348
 KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 379)
AUTHORS Akimura,T., Arikawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Koude,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takehashi,F., Takeku-Akaike,S., Tanaka,T., Tomaru,A., Toya,T., Watanabe,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
TITLE Unpublished (2001)
JOURNAL Contact: Yoshinide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuyama,H., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.
FEATURES
source
1. 379
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="G630034P22"
/clone_lib="RIKEN full-length enriched, adult male accessory axillary lymph node"
/sex="male"
/tissue_type="accessory axillary lymph node"
/dev_stage="adult"
/note="pooled tissues: (tissue_type=cerebellum, dev_stage=16 days neonate, sex=mixed), (tissue_type=cerebellum, dev_stage=0 day neonate, sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=male), (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days embryo, sex=mixed)"
BASE COUNT 84 a 97 c 93 g 105 t
ORIGIN
Query Match 73.7%; Score 267.6; DB 10; Length 379;
Best Local Similarity 93.6%; Pred. No. 6.3e-72;
Matches 279; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 CAGGTACTCTGAAAGAGCTGGCCCTGGGATATTCAGAGCCGCCAGACCTCAGATCG 60
DB 79 CAGGTACTCTGAAAGAGCTGGCCCTGGGATATTCAGAGCCGCCAGACCTCAGATCG 138

QY 61 ACTGTTCTTCTCTGGGTTTTCAGTACGACCTTCGTATGGGTGTGAGCTGGATTGCA 120
DB 139 ACTGTTCTTCTCTGGGTTTTCAGTACGACCTTCGTATGGGTGTGAGCTGGATTGCA 198
QY 121 CAGCTTCAGAGGAAGGCTCTGAGAGTGGCTGGCACACATTACTGCGATGACACAGCC 180
DB 199 CAGCTTCAGAGGAAGGCTCTGAGAGTGGCTGGCACACATTACTGCGATGATAGTAC 258
QY 181 TATACCCATCCCTGAAGAGCCGCTTACATCTCCAGAGTACCTCCACACAGAGTA 240
DB 259 TATACCCATCCCTGAAGAGTGGCTTACATCTCCAGAGTACCTCCACACAGAGTA 318
QY 241 TTCCCTCAAGATCAGCAGTGTGACACTGAGATATGCGACATATCTAGTGTGCGAA 298
DB 319 TTCCCTCAAGATCAGCAGTGTGACACTGAGATATCTAGTGTGCGAA 376
RESULT 10
BB870162
LOCUS
DEFINITION
BB870162 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630018N20 5', mRNA sequence.
ACCESSION
BB870162
VERSION
BB870162.1 GI:171116372
KEYWORDS
EST.
SOURCE
house mouse.
MUS MUSCULUS
ORGANISM
Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 363)
AUTHORS Akimura,T., Arikawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Koude,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takehashi,F., Takeku-Akaike,S., Tanaka,T., Tomaru,A., Toya,T., Watanabe,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
TITLE Unpublished (2001)
JOURNAL Contact: Yoshinide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuyama,H., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.
FEATURES
source
1. 363
Location/Qualifiers

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_1lb="RIKEN full-length enriched, adult male
accessory axillary lymph node"
/sex="male"
/tissue_type="accessory axillary lymph node"
/dev_stage="adult"
/note="pooled tissues: (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"
BASE COUNT      79 a      93 c      90 g      101 t
ORIGIN

```

```

Query Match      72.3% Score 262.6; DB 10; Length 363;
Best Local Similarity 93.5% Pred. No. 2.2e-70;
Matches 274; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```

```

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATTTGACGCCCTCCAGACCTCAGTCTG 60
DB 71 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATTTGACGCCCTCCAGACCTCAGTCTG 130
QY 61 ACTTGTCTTCTCTCTGGGTTTTCACATGACACTTCTGTAGTGTGAGTGTGATTCGA 120
DB 131 ACTTGTCTTCTCTCTGGGTTTTCACATGACACTTGTGTAGTGTGAGTGTGATTCGT 190
QY 121 CAGCCTTCAGGAAGAGGTCTGAGTGTGCTGGACACATTTACTGGATGATGATGACGC 180
DB 191 CAGCCTTCAGGAAGAGGTCTGAGTGTGCTGGACACATTTGTGTGATGATGATGATAC 250
QY 181 TATTAACCATCCCTGAGAGAGCGGCTTACATCTCCAGATATCTCCAGACACAGGTA 240
DB 251 TATTAACCATCCCTGAGAGAGCGGCTTACATCTCCAGATATCTCCAGACACAGGTA 310
QY 241 TTCTCTCAAGATCCCAATGTGGACATCGATATCTCCATCTACTGTGC 293
DB 311 TTCTCTCAAGATCCCAATGTGGACATCGATATCTCCATCTACTGTGC 363

```

```

RESULT 11
LOCUS      BB870127      366 bp      mRNA      linear      EST 27-NOV-2001
DEFINITION BB870127 RIKEN full-length enriched, adult male accessory axillary
            lymph node Mus musculus cDNA clone G630018121 5', mRNA sequence.
ACCESSION  BB870127
VERSION     BB870127.1 GI:17116337
KEYWORDS   EST.
SOURCE     house mouse.
            Mus musculus
ORGANISM   Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 366)

```

```

REFERENCE  1 (bases 1 to 366)
AUTHORS   Altamura,T., Arakawa,T., Carninci,P., Furuno,M., Hangaki,T.,
            Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii
            Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
            Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            A., Takahashi,F., Takaku-Akehira,S., Tanaka,T., Tomaru,A., Toyata,
            T., Watanuki,A., Yasunishi,A., Yamamatsu,M., and Hayashizaki,T.
            RIKEN Encyclopedia of Mouse Full-length cDNAs (AKimura,T., et al.
            2001)

```

```

JOURNAL   Unpublished (2001)
COMMENT   Contact: Yoshinide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

```

```

Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Iwata,M., Ohara,E.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencing. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukushima,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y., and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

```

FEATURES

```

source
location/Qualifiers
1..366
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_1lb="G630018121"
/clone_1lb="RIKEN full-length enriched, adult male
accessory axillary lymph node"
/sex="male"
/tissue_type="accessory axillary lymph node"
/dev_stage="adult"
/note="pooled tissues: (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"
BASE COUNT      80 a      94 c      91 g      101 t
ORIGIN

```

```

Query Match      72.3% Score 262.4; DB 10; Length 366;
Best Local Similarity 92.9% Pred. No. 2.5e-70;
Matches 275; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```

```

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATTTGACGCCCTCCAGACCTCAGTCTG 60
DB 71 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATTTGACGCCCTCCAGACCTCAGTCTG 130
QY 61 ACTTGTCTTCTCTCTGGGTTTTCACATGACACTTCTGTAGTGTGAGTGTGATTCGA 120
DB 131 ACTTGTCTTCTCTCTGGGTTTTCACATGACACTTCTGTAGTGTGAGTGTGATTCGT 190
QY 121 CAGCCTTCAGGAAGAGGTCTGAGTGTGCTGGACACATTTACTGGATGATGATGACGC 180
DB 191 CAGCCTTCAGGAAGAGGTCTGAGTGTGCTGGACACATTTGTGTGATGATGATGATAC 250
QY 181 TATTAACCATCCCTGAGAGAGCGGCTTACATCTCCAGATATCTCCAGACACAGGTA 240
DB 251 TATTAACCATCCCTGAGAGAGCGGCTTACATCTCCAGATATCTCCAGACACAGGTA 310
QY 241 TTCTCTCAAGATCCCAATGTGGACATCGATATCTCCATCTACTGTGTGC 296
DB 311 TTCTCTCAAGATCCCAATGTGGACATCGATATCTCCATCTACTGTGTGC 366

```

```

RESULT 12
LOCUS      AA880491      438 bp      mRNA      linear      EST 26-MAR-1998

```

DEFINITION vx40h05.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone
IMAGE:127721 5' similar to gb:S69331_cds1 IG HEAVY CHAIN V-II
REGION (HUMAN); mRNA sequence.

ACCESSION AA880491
VERSION AA880491.1 GI:2989474
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 438)
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steple, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maira M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
NCI:669521
Seq primer: -28ml3 rev1 ET from Amersham.

FEATURES
Source
Location/Qualifiers
1. 438
/organism="Mus musculus"
/strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
/clone="IMAGE:127721"
/clone_1lb="Stratagene mouse lung 937302"
/sex="female"
/tissue="lung"
/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: lung; Vector: plasmid SK-; Site: 1; Score
dt: 6-8 month old female lung and 1.5 year old male lung
were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP
XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT 104 a 113 c 91 g 130 t
ORIGIN
Query Match 71.8%; Score 260.6; DB 9; Length 438;
Best Local Similarity 84.5%; Pred. No. 9.8e-70;
Matches 305; Conservative 0; Mismatches 54; Indels 2; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCGGATATTTGAGCCCTCCGAGCCCTCAGCTG 60
Db 80 CAGGTACTCTGAAAGAGTCTGGCCCGGATATTTGAGCCCTCCGAGCCCTCAGCTG 139
QY 61 ACTGTCTTCTCTCTGGGTTTCACTGAGCACTTGTGATGGGTGAGCTGATTCGA 120
Db 140 ACTGTCTTCTCTCTGGGTTTCACTGAGCACTTGTGATGGGTGAGCTGATTCG 199
QY 121 CAGCTTCAAGAAAGGTCTGAGTGGCTGGCAGACATTTAGTGGATGATGACAGCC 180
Db 200 CAGCTTCAAGAAAGGTCTGAGTGGCTGGCAGACATTTAGTGGATGATGATAT 259
QY 181 TATTAACCATCTGTAAGAGCGGCTTACAACTCCAAAGATACCTCCAGACCGGTA 240
Db 260 TATTAACCATCTGTAAGAGCGGCTTACAACTCCAAAGATACCTCCAGACCGGTA 319
QY 241 TTCTCAAGATCAACAGTGTGAGACTGAGATCTGACATCTGACATCTGCTGCAAG 300
Db 320 TTCTCAAGATCAACAGTGTGAGATCTGACATCTGACATCTGCTGCTGCAAG 379

QY 301 GTCTCTTACTGCTATGCTATGAGTACTGAGGCTCAGGAACCTCAGTACCGCTCC 360
Db 380 G--AAACTACGAGTACTGACTGCTACTGAGGCGCAAGCAGCCTTACACAGCTCC 437

QY 361 T 361
Db 438 T 438

RESULT 13
LOCUS BF581194
DEFINITION 900 bp mRNA linear EST 12-DEC-2000
602100390F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:422011 5',
mRNA sequence.
ACCESSION BF581194
VERSION BF581194.1 GI:11654906
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 900)
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: L1A8803 row: C column: 24
High quality sequence stop: 639.

FEATURES
Source
Location/Qualifiers
1. 900
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:422011"
/clone_1lb="NCI_CGAP_C024"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPOX6; Site: 1; Note:
Site: 2; Sali; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 211 a 237 c 232 g 220 t
ORIGIN
Query Match 71.6%; Score 259.8; DB 12; Length 900;
Best Local Similarity 84.6%; Pred. No. 2.3e-69;
Matches 307; Conservative 0; Mismatches 47; Indels 9; Gaps 1;

QY 1 CAGGTACTCTGAAAGAGTCTGGCCCGGATATTTGAGCCCTCCGAGCCCTCAGCTG 60
Db 56 CAGGTACTCTGAAAGAGTCTGGCCCGGATATTTGAGCCCTCCGAGCCCTCAGCTG 115
QY 61 ACTGTCTTCTCTCTGGGTTTCACTGAGCACTTGTGATGGGTGAGCTGATTCGA 120
Db 116 ACTGTCTTCTCTCTGGGTTTCACTGAGCACTTGTGATGGGTGAGCTGATTCG 175
QY 121 CAGCTTCAAGAAAGGTCTGAGTGGCTGGCAGACATTTAGTGGATGATGACAGCC 180
Db 176 CAGCTTCAAGAAAGGTCTGAGTGGCTGGCAGACATTTAGTGGATGATGATAGTAC 235
QY 181 TATTAACCATCTGTAAGAGCGGCTTACAACTCCAAAGATACCTCCAGACCGGTA 240
Db 236 TATTAACCATCTGTAAGAGCGGCTTACAACTCCAAAGATACCTCCAAAGTAC 295
QY 241 TTCTCAAGATCAACAGTGTGAGACTGAGATCTGACATCTGACATCTGCTGCAAG 300
Db 241 TTCTCAAGATCAACAGTGTGAGACTGAGATCTGACATCTGACATCTGCTGCAAG 300

Db 296 TTCCTGAAGATCCGACACTGTGACACTGACAGATCTCCATATATATCTGCTCG- 351

QY 301 GTCCTCTACTGCTGCTATGCTATGCTAGCTGGGCTGACAGACCTCAGTCCGCTCC 360

Db 352 -----CCGAAGTAACTGGAGCTTTGACTACTGGGCGCAAGGACCACTCTCAGTCTCC 406

QY 361 TCA 363

Db 407 TCA 409

RESULT 14

BB873796 377 bp mRNA linear EST 27-NOV-2001

LOCUS BB873796 RIKEN full-length enriched adult male accessory axillary

DEFINITION lymph node Mus musculus cDNA clone G630050003 5', mRNA sequence.

ACCESSION BB873796.1 GI:17120006

VERSION BB873796.1

KEYWORDS EST.

ORGANISM Mus musculus.

house mouse.

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 377)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hirose, K., Hirose, T., Hirose, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watabiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

Unpublished (2001)

Contact: Yoshinide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-32 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagii, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

Source

Location/Qualifiers

1..377

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="G630050003"

/clone_lib="RIKEN full-length enriched, adult male accessory axillary lymph node"

/sex="male"

/tissue_type="accessory axillary lymph node"

/dev_stage="adult"

/note="pooled tissues: (tissue_type=cerebellum, dev_stage=16 days neonate, sex=mixed), (tissue_type=cerebellum, dev_stage=0 day neonate, sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=male), (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days embryo, sex=mixed)"

BASE COUNT 79 a 93 c 100 g 105 t

ORIGIN

Query Match 71.5%: Score 259.6; DB 10; Length 377;

Best Local Similarity 91.9%: Pred. No. 1.9e-69;

Matches 274; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 CAGGTTACTGTGAAGAGTCTGGCCCTGGGATATTCGAGCCCTCCAGACCTCAGTCTG 60

Db 69 CAGGTTACTGTGAAGAGTCTGGCCCTGGGATATTCGAGCCCTCCAGACCTCAGTCTG 128

QY 61 ACTTGTCTTCTCTCTGGGTTTCTACCTGACACTCTCTGTATGGTGTGAGCTGATCGA 120

Db 129 ACTTGTCTTCTCTCTGGGTTTCTACCTGACACTCTCTGTATGGTGTGAGCTGATCGT 188

QY 121 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGCACACATTACTGGATGATGACAAAGCG 180

Db 189 CAGCCTTCAGGAAAGGCTCTGAGTGGCTGGCACACATTACTGGATGATGATGATGATG 248

QY 181 TATTAACCATCCTGGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGACACAGGTA 240

Db 249 TATTAACCATCCTGGAAGAGCGGCTTACATCTCCAAAGATACCTCCAAAGATACCTCC 308

QY 241 TTCCTGAAGATCCGACACTGTGACACTGACAGATCTCCATATATATCTGCTCGAA 298

Db 309 TTCCTGAAGATCCGACACTGTGACACTGACAGATCTCCATATATCTGCTCGAA 366

RESULT 15

AZ882936 589 bp DNA linear GSS 05-MAR-2001

LOCUS AZ882936

DEFINITION RPCI-23-187A23.TV RPCI-23 Mus musculus genomic clone RPCI-23-187A23

ACCESSION AZ882936

VERSION AZ882936.1 GI:13201881

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 589)

Zhao, S., Nieman, W., Feldblum, T., Malek, J., Shatsman, S., Akiret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSS: RPCI-23-187A23.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tftp/bac_ends/mouse/bac_end_intro.html

Plate: 187 row: A column: 23

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..589

FEATURES

Source

```
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone_1b="RPCI-23-187A23"  
/sex="Female"  
/lab_host="DH10B"  
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:  
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Size  
selected DNA was cloned into the pBAC3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."  
BASE COUNT      142 a      160 c      123 g      164 t  
ORIGIN
```

```
Query Match      71.5%; Score 259.6; DB 17; Length 589;  
Best Local Similarity 91.9%; Pred. No. 2.2e-69;  
Matches 274; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
  
1 CAGGTTACTCTGAAGAGTGTGGCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
|||  
Db      284 CAGGTTACTCTGAAGAGTGTGGCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 343  
|||  
  
61 ACTTGTCTCTCTCTGCGTTTTCACGTAGACACTTCTGTATGGGTGTGAGCTGATTCGA 120  
|||  
Db      344 ACTTGTCTCTCTCTGCGTTTTCACGTAGACACTTCTGTATGGGTGTGAGCTGATTCGT 403  
|||  
  
121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTCTGCGATGATGACAAAGCC 180  
|||  
Db      404 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTCTGCGATGATGATAGTAC 463  
|||  
  
181 TATACCCATCCCTGTAAGACCGGCTTACATCTCCAAAGGATATCTCCAGCAACAGGTA 240  
|||  
Db      464 TATACCCATCCCTGTAAGACCGGCTTACATCTCCAAAGGATATCTCCAGCAACAGGTT 523  
|||  
  
241 TTCTCAAGATCACAGTGTGACACTCGAGATACAGCAATCTACTACTGTGCTCGAA 298  
|||  
Db      524 TTCTCAAGATCACAGTGTGACACTCGAGATACAGCAATCTACTACTGTGCTCGAA 581  
|||
```

Search completed: July 10, 2003, 23:22:23
Job time : 1749 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:38:52 ; Search time 27 Seconds

(Without alignments)
131.858 Million cell updates/sec

Title: US-09-759-112A-7

Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSTL.....SLFAYAMDYMGQGSIVYSS 121

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	569	89.9	140	2	US-08-483-636-4		Sequence 4, Appl1
	2	569	89.9	140	2	US-08-483-632-4		Sequence 4, Appl1
	3	569	89.9	141	2	US-08-483-636-10		Sequence 10, Appl
	4	569	89.9	141	2	US-08-483-632-10		Sequence 10, Appl
	5	567.5	89.7	246	1	US-08-197-834-7		Sequence 7, Appl1
	6	551.5	87.1	122	1	US-08-436-463-14		Sequence 14, Appl
	7	522.5	82.5	139	5	PCT-US95-07372-10		Sequence 10, Appl
	8	521.5	82.4	120	2	US-09-553-501A-88		Sequence 88, Appl
	9	521.5	82.4	120	3	US-09-205-231-88		Sequence 88, Appl
	10	521.5	82.4	139	2	US-08-553-501A-29		Sequence 29, Appl
	11	521.5	82.4	139	3	US-09-205-231-29		Sequence 29, Appl
	12	506.5	80.0	120	2	US-08-290-592E-32		Sequence 32, Appl
	13	505.5	79.9	143	1	US-08-436-463-2		Sequence 2, Appl1
	14	504	79.6	108	1	US-08-436-463-17		Sequence 17, Appl
	15	502	79.3	141	2	US-08-483-636-12		Sequence 12, Appl
	16	502	79.3	141	2	US-08-483-632-12		Sequence 12, Appl
	17	500	79.0	121	2	US-08-483-636-64		Sequence 64, Appl
	18	500	79.0	121	2	US-08-483-632-64		Sequence 64, Appl
	19	499.5	78.9	120	5	PCT-US95-10053-29		Sequence 29, Appl
	20	499.5	78.9	120	5	PCT-US96-09448-32		Sequence 32, Appl
	21	499	78.8	108	1	US-08-436-463-15		Sequence 15, Appl
	22	489.5	77.3	120	5	PCT-US95-10053-28		Sequence 28, Appl
	23	489.5	77.3	120	5	PCT-US96-09448-31		Sequence 31, Appl
	24	482	76.1	114	1	US-08-436-463-16		Sequence 16, Appl
	25	470.5	74.3	126	4	US-09-225-322B-4		Sequence 4, Appl
	26	470.5	74.3	141	4	US-09-225-322B-4		Sequence 2, Appl
	27	467.5	73.9	120	2	US-08-290-592E-31		Sequence 31, Appl

28	459.5	72.6	120	4	US-09-025-769B-23	Sequence 23, Appl
29	454	71.7	121	4	US-09-025-769B-37	Sequence 37, Appl
30	454	71.7	121	4	US-09-025-769B-61	Sequence 61, Appl
31	445	70.3	123	5	PCT-US95-10053-27	Sequence 27, Appl
32	445	70.3	123	5	PCT-US96-09448-30	Sequence 30, Appl
33	443	70.0	499	4	US-09-049-672A-1	Sequence 1, Appl
34	440.5	69.6	139	2	US-08-553-501A-59	Sequence 59, Appl
35	440.5	69.6	139	2	US-09-205-231-59	Sequence 59, Appl
36	437.5	69.1	139	2	US-08-553-501A-61	Sequence 61, Appl
37	437.5	69.1	139	2	US-09-205-231-61	Sequence 61, Appl
38	436	68.9	123	3	US-08-290-592E-30	Sequence 30, Appl
39	433.5	68.5	120	2	US-08-553-501A-90	Sequence 90, Appl
40	433.5	68.5	120	3	US-09-205-231-90	Sequence 90, Appl
41	431.5	68.2	141	2	US-08-345-321-10	Sequence 10, Appl
42	430.5	68.0	120	2	US-08-553-501A-91	Sequence 91, Appl
43	430.5	68.0	120	3	US-09-205-231-91	Sequence 91, Appl
44	422.5	66.7	128	2	US-08-428-197-15	Sequence 15, Appl
45	422.5	66.7	128	5	PCT-US93-10555-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-4
Sequence 4, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TREATMENT OF IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-483-636-4

Query Match 89.9%; Score 569; DB 2; Length 140;
Best Local Similarity 90.1%; Pred. No. 4.6e-50;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILPQSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKGLEMLAHYWDKKR 60
DB 20 QVTLKESGPGILPQSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKGLEMLAHYWDKKR 79
QY 61 YNPSLKSRLLTSKNTSSNOVFLKITSVDFTATYYCARRVSLTAYAMDYWGOSTVTVS 120
DB 80 YNPSLKSRLLTSKNTSSNOVFLKITSVDFTATYYCARRVSLTAYAMDYWGOSTVTVS 139
QY 121 S 121
DB 140 S 140

RESULT 2
US-08-483-632-4
Sequence 4, Application US/08483632
Patent No. 5928904

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-4

Query Match 89.9%; Score 569; DB 2; Length 140;
Best Local Similarity 90.1%; Pred. No. 4.6e-50;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILPQSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKGLEMLAHYWDKKR 60
DB 20 QVTLKESGPGILPQSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKGLEMLAHYWDKKR 79
QY 61 YNPSLKSRLLTSKNTSSNOVFLKITSVDFTATYYCARRVSLTAYAMDYWGOSTVTVS 120
DB 80 YNPSLKSRLLTSKNTSSNOVFLKITSVDFTATYYCARRVSLTAYAMDYWGOSTVTVS 139
QY 121 S 121
DB 140 S 140

RESULT 3
US-08-483-636-10
Sequence 10, Application US/08483636
Patent No. 5914110

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful In
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-10

Query Match 89.9%; Score 569; DB 2; Length 141;
Best Local Similarity 90.1%; Pred. No. 4.7e-50;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILPQSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKGLEMLAHYWDKKR 60
|||||

Db 21 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHIIYDDDKR 80
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYANDYWGQGTSTVVS 120
Db 81 YNPSLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYANDYWGQGTSTVVS 140
QY 121 S 121
Db 141 S 141

RESULT 4
US-08-483-632-10

; Sequence 10, Application US/08483632
; Patent No. 5928904

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/483,632

APPLICATION DATA:

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

*APPLICATION NUMBER: US 08/117366

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783

FILING DATE: 14-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 141 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-632-10

Query Match 89.9%; Score 569; DB 2; Length 141;

Best Local Similarity 90.1%; Pred. No. 4.7e-50;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHIIYDDDKR 60
Db 21 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHIIYDDDKR 80
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYANDYWGQGTSTVVS 120
Db 81 YNPSLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYANDYWGQGTSTVVS 140

Db 81 YNPSLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYANDYWGQGTSTVVS 140
QY 121 S 121
Db 141 S 141

RESULT 5
US-08-197-834-7

; Sequence 7, Application US/08197834
; Patent No. 5639455

GENERAL INFORMATION:

APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESSES:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,834

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 028173/1993

FILING DATE: 17-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5639455man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-661-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-197-834-7

Query Match 89.7%; Score 567.5; DB 1; Length 246;

Best Local Similarity 89.6%; Pred. No. 1.3e-49;

Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHIIYDDDKR 60
Db 123 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPCKGLEMLAHIIYDDDKR 182
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYANDYWGQGTSTVVS 116
Db 183 YNPSLKSRLTISKDTSSNQVFLKITSVDPRTATYYCARVSLTYANDYWGQGTSTVVS 241
QY 117 VTVSS 121
Db 242 VTVSS 246

RESULT 6
US-08-436-463-14

; Sequence 14, Application US/08436463

Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuniko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-14

Query Match 87.1%; Score 551.5; DB 1; Length 122;
Best Local Similarity 91.4%; Pred. No. 2.2e-48;
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Db 1 QVTLKESGPGILQPSQTLTLCSFSGSLTSGMGVSMIROPSCGLEMIAHIYWDK 60
8 QVTLKESGPGILQPSQTLTLCSFSGSLTSGMGVSMIROPSCGLEMIAHIYWDK 67

QY 61 YNPSLKRLTISKDTSSNOVFLKITSVDTPTATYCCARRVSLTAVAMDYGOSTS 116
DB 68 YNPSLKRLTISKDTSSNOVFLKITSVDTPTATYCCARRVSLTAVAMDYGOSTS 122

RESULT 7
PCT-US95-07372-10
Sequence 10, Application PC/TUS9507372
GENERAL INFORMATION:
APPLICANT: Oklahoma Medical Research Foundation
TITLE OF INVENTION: Calcium Binding Recombinant
TITLE OF INVENTION: Antibody Against Protein C
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07372
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF106CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: HPC-4 Heavy Chain Variable Region (YH Gamma)
FEATURE:
NAME/KEY: misc-feature
LOCATION: 20..139
OTHER INFORMATION: /note= "Gln' at position 20 starts
OTHER INFORMATION: mature peptide."
PCT-US95-07372-10

Query Match 82.5%; Score 522.5; DB 5; Length 139;
Best Local Similarity 84.3%; Pred. No. 2.1e-45;
Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLTLCSFSGSLTSGMGVSMIROPSCGLEMIAHIYWDK 60
DB 20 QVTLKESGPGILQPSQTLTLCSFSGSLTSGMGVSMIROPSCGLEMIAHIYWDK 79

QY 61 YNPSLKRLTISKDTSSNOVFLKITSVDTPTATYCCARRVSLTAVAMDYGOSTS 120
DB 80 YNPSLKRLTISKDTSSNOVFLKITSVDTPTATYCCARRVSLTAVAMDYGOSTS 138

QY 121 S 121
DB 139 S 139

RESULT 8
US-08-553-501a-88
Sequence 88, Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATE: 20-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-553-501A-88

Query Match 82.4%; Score 521.5; DB 2; Length 120;
Best Local Similarity 83.7%; Pred. No. 2.2e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQSPQTLSTLCFSFGFSLSTSGMGVSWIRPSPGKGLMLAHIIYWDKKR 60
DB 1 QVTLKESGPGILQSPQTLSTLCFSFGFSLSTSGMGVSWIRPSPGKGLMLAHIIYWDKKY 60
QY 61 YNPSLKSLTISKDPSNQVFLKITSVDRPTATYTCARVSLFAY--AMDYWGQGSTVT 118
DB 61 YNPALKGRLTISKDPSNQVFLKITSVDRPTATYTCARVSLFAY--AMDYWGQGSTVT 117

QY 119 VSS 121
DB 118 VSS 120

RESULT 9

US-09-205-231-88

Sequence 88, Application US/09205231

Patent No. 6121423

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/205,231

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-205-231-88

Query Match 82.4%; Score 521.5; DB 3; Length 120;
Best Local Similarity 83.7%; Pred. No. 2.2e-45;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQSPQTLSTLCFSFGFSLSTSGMGVSWIRPSPGKGLMLAHIIYWDKKR 60
DB 1 QVTLKESGPGILQSPQTLSTLCFSFGFSLSTSGMGVSWIRPSPGKGLMLAHIIYWDKKY 60
QY 61 YNPSLKSLTISKDPSNQVFLKITSVDRPTATYTCARVSLFAY--AMDYWGQGSTVT 118
DB 61 YNPALKGRLTISKDPSNQVFLKITSVDRPTATYTCARVSLFAY--AMDYWGQGSTVT 117

QY 119 VSS 121
DB 118 VSS 120

RESULT 10

US-08-553-501A-29

Sequence 29, Application US/08553501A

Patent No. 5856135

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,501A

FILING DATE: 20-FEB-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP94/00859

FILING DATE: 30-MAY-1994

CLASSIFICATION: JP 5-129787

PRIOR APPLICATION DATA:

TELECOMMUNICATION INFORMATION:

Query Match 80.0%; Score 506.5; DB 2; Length 120;

Best Local Similarity 81.8%; Pred. No. 7.2e-44;
Matches 99; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Oy 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIRPSPGKLEMLAHIIYWDKDR 60
Db 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIRPSPGKLEMLAHIIYWDKDR 60
Oy 61 YNPSLKRSLTISKRTSSNOVFLKITSVDTRATATYTCARRVSLTAYAMDYGOGTSYTVS 120
Db 61 YNPSLKRSLTISKRTSSNOVFLKITSVDTRATATYTCARRVSLTAYAMDYGOGTSYTVS 119

Oy 121 S 121
Db 120 S 120

RESULT 13
US-08-436-463-2
Sequence 2, Application US/08436463
Patent No. 5760185

GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoaki
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-BODY AND GENE FRAGMENT CODING FOR SAID ANTI-BODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 143 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-2

Query Match 79.9%; Score 505.5; DB 1; Length 143;
Best Local Similarity 79.8%; Pred. No. 1.1e-43;
Matches 99; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

Oy 1 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIRPSPGKLEMLAHIIYWDKDR 60
Db 20 QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIRPSPGKLEMLAHIIYWDKDR 79

Oy 61 YNPSLKRSLTISKRTSSNOVFLKITSVDTRATATYTCARRVSLTAYAMDYGOGTSYTVS 117
Db 80 YNPSLKRSLTISKRTSSNOVFLKITSVDTRATATYTCARRVSLTAYAMDYGOGTSYTVS 139

Oy 118 TVSS 121
Db 140 TVSA 143

RESULT 14
US-08-436-463-17

Sequence 17, Application US/08436463
Patent No. 5760185

GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoaki
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-BODY AND GENE FRAGMENT CODING FOR SAID ANTI-BODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-17

Query Match 79.6%; Score 504; DB 1; Length 108;
Best Local Similarity 90.8%; Pred. No. 1.1e-43;
Matches 99; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

Oy 9 PGIQPSQTLSTLCFSFGSLSTSGMGVSWIRPSPGKLEMLAHIIYWDKDRYNSPKSR 68
Db 1 PGIQPSQTLSTLCFSFGSLSTSGMGVSWIRPSPGKLEMLAHIIYWDKDRYNSPKSR 59

Oy 69 LTISKRTSSNOVFLKITSVDTRATATYTCARRVSLTAYAMDYGOGTSYTVS 116
Db 60 LTISKRTSSNOVFLKITSVDTRATATYTCARRVSLTAYAMDYGOGTSYTVS 108

RESULT 15
US-08-483-636-12

Sequence 12, Application US/08483636
Patent No. 5914110

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.

Mouse heavy chain
Human IgG1 antibody
MO99373630 Seq ID 3
Antiviral scFv-anti-
TmV 34K protein-anti-
Mouse antibody 13G8
Protein #2 in lane
Anti-RSV F glycopro-
Sequence of mouse
Humanized antibody
Heavy chain variablb
Heavy chain sequenc
Heavy chain variabl
Heavy chain sequen
Rat immunoglobulin
KM50 cell-derived
KM50 Rat immunogl
Rat activated immu
Humanised antibody
Mouse anti-RSV ant
COD-grafted anti-R
Anti-RSV antibody
Anti-RSV antibody
Anti-RSV antibody
Anti-RSV antibody
Anti-RSV antibody
Humanised antibody
Humanised high pot
Humanised high pot
Humanised high pot
Humanised high pot
Human Ab heavy cha
Humanised high pot
Humanised high pot
Humanised high pot

XX 07-SEP-1993; 9305-0117366.
 PR 14-OCT-1993; 9305-0136783.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Gross MS, Holmes SD, Sylvester DR.
 PI Gross MS, Holmes SD, Sylvester DR.
 DR N-PSDB; AA083491.
 XX WPI; 1995-123387/16.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
 from high affinity mabs - useful in treatment of IL-4-mediated
 PT and IGE-mediated allergic conditions
 PS Disclosure; Fig.2; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. CDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (AA083490-91), and used for
 CC antibody engineering.
 XX Sequence 140 AA:
 SQ
 Query Match 89.9%; Score 569; DB 16; Length 140;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKSGPQIIQPSQTLSTLCSPGFSLSSTSGMGVSWINQPSGKGLHIAHYMDDDR 60
 DB 20 QVTLKSGPQIIQPSQTLSTLCSPGFSLSSTSGMGVSWINQPSGKGLHIAHYMDDDR 79
 QY 61 YNPSLKSRLTISKDTSSNOVFELKITSVDPTATYTCARVSLTAYAMDYGQGTSTVTS 120
 DB 80 YNPSLKSRLTISKDTSSNOVFELKITSVDPTATYTCARVSLTAYAMDYGQGTSTVTS 139
 QY 121 S 121
 DB 140 S 140
 RESULT 2
 AA123768
 ID AAY23768 standard; Protein; 140 AA.
 XX AAY23768;
 C 13-SEP-1999 (first entry)
 DE Heavy chain variable region of murine IL-4 antibody 3B9.
 XX Heavy chain variable region of murine IL-4 antibody 3B9.
 DE Heavy chain variable region of murine IL-4 antibody 3B9.
 XX Heavy chain variable region of murine IL-4 antibody 3B9.
 KW chimeric antibody: humanised antibody; IL-4 mediated allergic reaction;
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;
 KW allergy.
 XX Mus sp.
 OS
 XX US5928904-A.
 PN 27-JUL-1999.
 PD 27-JUL-1999.
 XX 07-JUN-1995; 9505-0483632.
 PF 07-JUN-1995; 9505-0483632.
 XX 07-JUN-1995; 9505-0483632.
 PR 07-SEP-1993; 9305-0117366.
 PR 14-OCT-1993; 9305-0136783.
 PR 07-SEP-1994; 94WO-US10308.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Gross MS, Holmes SD, Sylvester DR.
 PI Gross MS, Holmes SD, Sylvester DR.
 DR N-PSDB; AA083491.
 XX WPI; 1995-123387/16.
 PT Chimeric and humanised IL-4 monoclonal antibodies (mabs), derived
 from high affinity mabs - useful in treatment of IL-4-mediated
 PT and IGE-mediated allergic conditions
 PS Disclosure; Fig.2; 97pp; English.
 CC Spleen cells from mice immunized with human IL-4 were used to prepare
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only
 CC clone 3B9 was positive. CDNA clones of the 3B9 light and heavy
 CC chains were cloned into pGEM7f and transformed into E. coli
 CC DH5-alpha. The clones were sequenced (AA083490-91), and used for
 CC antibody engineering.
 XX Sequence 140 AA:
 SQ
 Query Match 89.9%; Score 569; DB 20; Length 140;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKSGPQIIQPSQTLSTLCSPGFSLSSTSGMGVSWINQPSGKGLHIAHYMDDDR 60
 DB 20 QVTLKSGPQIIQPSQTLSTLCSPGFSLSSTSGMGVSWINQPSGKGLHIAHYMDDDR 79
 QY 61 YNPSLKSRLTISKDTSSNOVFELKITSVDPTATYTCARVSLTAYAMDYGQGTSTVTS 120
 DB 80 YNPSLKSRLTISKDTSSNOVFELKITSVDPTATYTCARVSLTAYAMDYGQGTSTVTS 139
 QY 121 S 121
 DB 140 S 140
 RESULT 3
 AA18121
 ID AAY18121 standard; Protein; 140 AA.
 XX AAY18121;
 AC 11-AUG-1999 (first entry)
 DE Heavy chain sequence for murine 3B9 antibody.
 XX Heavy chain sequence for murine 3B9 antibody.
 DE Heavy chain sequence for murine 3B9 antibody.
 XX Heavy chain sequence for murine 3B9 antibody.
 KW antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX Mus sp.
 OS
 XX US5914110-A.
 PN 22-JUN-1999.
 PD 22-JUN-1999.
 XX 07-JUN-1995; 9505-0483636.
 PF 07-JUN-1995; 9505-0483636.
 XX 07-JUN-1995; 9505-0483636.
 PR 07-SEP-1993; 9305-0117366.
 PR 14-OCT-1993; 9305-0136783.
 PR 07-SEP-1994; 94WO-US10308.

PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX WPI: 1999-370482/31.
 DR N-PSDB; AAY79520.
 XX
 PT Recombinant IL4 antibodies
 PS
 XX Claim 24; Fig 2; 50pp; English.
 PS
 CC This sequence represents the heavy chain of the murine 3B9
 CC antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 CC
 XX Sequence 140 AA;
 SQ
 Query Match 89.9%; Score 569; DB 20; Length 140;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDGDKR 60
 DB 20 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDGDKR 79
 QY 61 YNPSLKSRLLTISKDTSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDVGQSTYTVS 120
 DB 80 YNPSLKSRLLTISKDTSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDVGQSTYTVS 139
 QY 121 S 121
 DB 140 S 140
 Db
 RESULT 4
 AAR70191
 ID AAR70191 standard; Protein; 141 AA.
 XX
 AC AAR70191;
 XX
 XX 20-SEP-1995 (first entry)
 DE Chimeric antibody 3B9 heavy chain.
 XX
 KM Chimeric antibody; antibody engineering; monoclonal antibody;
 KM MAb; interleukin-4; IL-4; allergy.
 XX
 OS Homo sapiens; Mus sp.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..19
 FT /label= Sig-Peptide
 FT 51..57
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT 72..87
 FT /label= CDR
 FT /note= "complementarity determining region"
 FT 120..130
 FT /label= CDR
 FT /note= "complementarity determining region"
 XX
 PN MO9507301-A.
 XX 16-MAR-1995.
 PD
 XX

PF 07-SEP-1994; 94MO-US10308.
 XX
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX WPI: 1995-123387/16.
 DR N-PSDB; AAQ83492.
 XX
 PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
 PT from high affinity mAbs - useful in treatment of IL-4-mediated
 PT and IgE-mediated allergic conditions
 PS
 XX Disclosure; Fig.3; 97pp; English.
 CC
 CC A human/mouse chimeric antibody heavy chain variable region was
 CC constructed (given in AAR70191) that contained the mouse anti-human
 CC IL-4 Mab 3B9 variable region including 3 CDRs (AAR70198-200) and a
 CC human antibody signal peptide (AAR70193). The construct was used
 CC for humanized antibody production.
 CC
 XX Sequence 141 AA;
 SQ
 Query Match 89.9%; Score 569; DB 16; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDGDKR 60
 DB 21 QVTLKESGPGILQPSQTLSTLCSFSGSLSTSGMGVSMIRPSGKGLMLAHYWDGDKR 80
 QY 61 YNPSLKSRLLTISKDTSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDVGQSTYTVS 120
 DB 81 YNPSLKSRLLTISKDTSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDVGQSTYTVS 140
 QY 121 S 121
 DB 141 S 141
 Db
 RESULT 5
 AAY23769
 ID AAY23769 standard; Protein; 141 AA.
 XX
 AC AAY23769;
 XX
 XX 13-SEP-1999 (first entry)
 DE Heavy chain variable region of murine/human chimeric antibody 3B9.
 XX
 KM Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;
 KM chimeric antibody; humanised antibody; IL-4-mediated allergic reaction;
 KM immunoglobulin E-mediated allergic reaction; allergic rhinitis;
 KM conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;
 KM rheumatoid arthritis; host-versus-graft disease; renal disease;
 KM allergy.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN US5928904-A.
 XX
 PD 27-JUL-1999.
 XX
 PF 07-JUN-1995; 95US-0483632.
 XX
 PR 07-JUN-1995; 95US-0483632.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR

PR 07-SEP-1994; 94WO-US10308.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 DR WPI; 1999-429500/36.
 DR N-PSDB; AAX85886.
 XX
 PT New DNA molecules encoding recombinant antibodies useful for
 PT treating IL4-mediated conditions
 XX
 PS Example 3; Fig 3; 50pp; English.
 XX
 CC The present sequence represents the heavy chain variable region of
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The
 CC specification describes chimeric and humanised IL-4 monoclonal
 CC antibodies. The antibodies of the invention are used in therapeutic
 CC and pharmaceutical compositions for treating IL-4 mediated and
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.
 CC They are also useful in the diagnosis of an allergy or condition
 CC associated with excess IL-4 production through the measurement e.g. by
 CC ELISA of circulating endogenous IL-4 levels in humans.
 CC
 SQ Sequence 141 AA;

Query Match 89.9%; Score 569; DB 20; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGIILPQSOTLSITCSFSGFSLSTSGMGVSWIRPGSGLEMLAHYWDKKR 60
 DB 21 QVTLKESGPGIILPQSOTLSITCSFSGFSLSTSGMGVSWIRPGSGLEMLAHYWDKKR 80
 QY 61 YNPSLSRLTISKDTSSNOVFLKITSVDTRATYYCARRVSLTAYAMDYGGTSVTVS 120
 DB 81 YNPSLSRLTISKDTSSNOVFLKITSVDTRATYYCARRVSLTAYAMDYGGTSVTVS 140
 QY 121 S 121
 DB 141 S 141

RESULT 6
 AAY18125
 AAY18125 standard; Protein; 141 AA.

XX AAY18125;
 DT 11-AUG-1999 (first entry)
 XX
 DE Chimeric 3B9 monoclonal antibody heavy chain.
 XX
 KW Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;
 KW autoimmune disease; graft versus host disease.
 XX
 OS Synthetic.
 XX
 PN US5914110-A.
 XX
 PD 22-JUN-1999.
 XX
 PE 07-JUN-1995; 95US-0483636.
 XX
 PR 07-JUN-1995; 95US-0483636.
 PR 07-SEP-1993; 93US-0117366.
 PR 14-OCT-1993; 93US-0136783.
 PR 07-SEP-1994; 94WO-US10308.

XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gross MS, Holmes SD, Sylvester DR;
 XX
 DR WPI; 1999-370482/31.
 DR N-PSDB; AAX79542.
 XX
 PT Recombinant IL4 antibodies
 XX
 PS Example 5; Fig 3; 50pp; English.
 XX
 CC This sequence represents the light chain of the chimeric
 CC 3B9 antibody of the invention. The antibody is a chimeric or
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of
 CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for
 CC the treatment of allergic disorders such as allergic rhinitis,
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.
 CC The antibodies are also useful for regulating B and T cell proliferation
 CC and as such are useful in the treatment of autoimmune diseases and graft
 CC versus host disease.
 CC
 SQ Sequence 141 AA;

Query Match 89.9%; Score 569; DB 20; Length 141;
 Best Local Similarity 90.1%; Pred. No. 1.6e-48;
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGIILPQSOTLSITCSFSGFSLSTSGMGVSWIRPGSGLEMLAHYWDKKR 60
 DB 21 QVTLKESGPGIILPQSOTLSITCSFSGFSLSTSGMGVSWIRPGSGLEMLAHYWDKKR 80
 QY 61 YNPSLSRLTISKDTSSNOVFLKITSVDTRATYYCARRVSLTAYAMDYGGTSVTVS 120
 DB 81 YNPSLSRLTISKDTSSNOVFLKITSVDTRATYYCARRVSLTAYAMDYGGTSVTVS 140
 QY 121 S 121
 DB 141 S 141

RESULT 7
 AAR58612
 AAR58612 standard; Protein; 246 AA.

XX AAR58612;
 AC
 DT 28-APR-1995 (first entry)
 XX
 DE IL-6 binding inhibitor.
 XX
 KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
 KW septic shock; multiple myeloma; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP617126-A.
 XX
 PD 28-SEP-1994.
 XX
 PE 16-FEB-1994; 94EP-0102346.
 XX
 PR 17-FEB-1993; 93JP-0028173.
 XX
 PA (AJIN) AJINOKOTO KK.
 XX
 PI Hamuro J, Nakazawa H, Shimamura T;
 XX
 DR WPI; 1994-295777/37.
 DR N-PSDB; AAO70612.
 XX
 PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to

PT Its receptor - useful for treating auto-immune disease induced
 or aggravated by IL-6
 PS Claim 5; Page 18; 26pp; English.
 CC AAQ70612 codes for human interleukin-6 binding inhibitor, the
 CC polypeptide described in AAR58612. This polypeptide inhibits the
 CC binding of human IL-6 to its receptor, and can therefore be
 CC useful in the treatment of a variety of autoimmune diseases;
 CC specifically in the treatment of rheumatoid arthritis, septic
 CC shock due to bacterial infection and multiple myeloma.
 XX

Sequence 246 AA;

Query Match 89.7%; Score 567.5; DB 15; Length 246;
 Best Local Similarity 89.6%; Pred. No. 4.4e-48;
 Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWD DDKR 60
 |||
 123 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWD DDKH 182
 |||
 QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLA---YANDYWGQGSTS 116
 |||
 DB 183 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLA---YANDYWGQGSTS 241
 |||
 QY 117 VTSS 121
 |||
 DB 242 VTSS 246

RESULT 8

AAR54101 standard; Protein: 122 AA.

AA554101;

08-FEB-1995 (first entry)

Humanised MAb H-chain.

Human; mouse; murine; heavy; light; chain; monoclonal; antibody;
 complementarity determining region; CDR; IgG; kappa; IIIB; IIIM.

Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.

Key Location/Qualifiers
 Region 31..37
 /Label- CDR1
 Region 52..67
 /Label- CDR2
 Region 100..111
 /Label- CDR3

JP06141885-A.

24-MAY-1994.

05-NOV-1992; 92JP-0322476.

05-NOV-1992; 92JP-0322476.

(KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

WPI; 1994-205040/25.

N-PSDB; AAO68709.

Recombinant anti-HIV monoclonal antibody - capable of
 neutralising strains which can not be neutralised by anti-IIIB
 and IIIM antibodies
 Disclosure; Page 13; 23pp; Japanese.

XX The sequences given in AAR54101-02 represent the heavy and light chains
 CC respectively of the humanised monoclonal antibody (MAb) of the
 CC invention. The antibody has the ability to neutralise human
 CC immunodeficiency virus. The antibody is classified as IgG kappa and
 CC has the sequence RIGPGR or RVGPGR in the principal neutralising
 CC domain. The antibody may be used to neutralise the clinically
 CC separate strains which cannot be neutralised by the neutralising
 CC antibodies against IIIB and IIIM strains.
 XX

Sequence 122 AA;

Query Match 86.3%; Score 546.5; DB 15; Length 122;
 Best Local Similarity 87.7%; Pred. No. 2.3e-46;
 Matches 107; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWD DDKR 60
 |||
 DB 1 QVTLKESGPGILQPSQTLTLCSFSGFSLSTSGMGVSWIRPSGKGLMLAHYWD DDKH 60
 |||
 QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSL-TAYANDYWGQGSTVTV 119
 |||
 DB 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSL-TAYANDYWGQGSTVTV 120
 |||
 QY 120 SS 121
 |||
 DB 121 SS 122

RESULT 9

AAR88109 standard; peptide: 120 AA.

AAR88109;

25-JUL-1996 (first entry)

Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.

Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;
 zymogen; cleavage; mouse; humanised antibody; variable region;
 light chain; inhibition; anticoagulant; coagulation; tumour.

Mus musculus.

WO9534652-A1.

21-DEC-1995.

09-JUN-1995; 95WO-US07372.

10-JUN-1994; 94US-0259321.

(OKLA-) OKLAHOMA MED RES FOUND.

Esmon CT, Rezaie A;

WPI; 1996-049681/05.

N-PSDB; AAT09300.

Calcium-binding monoclonal antibody immunoreactive with Protein C -
 inhibits Protein C anticoagulant activation by
 thrombin-thrombomodulin, e.g. for treating tumours
 Claim 2; Page 29; 41pp; English.

This is the amino acid sequence of the mature peptide from the murine
 anti-protein C monoclonal antibody HPC-4 heavy chain variable region.
 HPC-4 recognises the activation peptide region (AAR88106) of the heavy
 chain of protein C, a vitamin K-dependent plasma protein zymogen.
 Protein C is converted to activated protein C (APC) by cleavage between
 the Arg-Leu amino acid contained within the activation peptide sequence.
 HPC-4 prevents protein C activation to APC by binding to this region.

CC The DNA sequences encoding the variable regions of the heavy and light
 CC chains of the antibody (AA09299-302) were used to construct humanised
 CC antibodies using the PCR primers AA09303-9. The humanised antibodies
 CC are useful as inhibitors of coagulation and can be used for the treatment
 CC of tumours by inhibiting the anticoagulant activity of APC by preventing
 CC conversion of protein C to APC.

XX Sequence 120 AA;

Query Match 82.5%; Score 522.5; DB 17; Length 120;
 Best Local Similarity 84.3%; Pred. No. 5.2e-44;
 Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILPSPQTLTSCSFGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60

DB 1 QVTLKESGPGILPSPQTLTSCSFGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60

QY 61 YNPGLKSRLLTISKDTSNQVFLKITSVDTRDTATYCCARRVSLTAYAMDYGOSTSVTVS 120
 DB 61 YNPGLKSRLLTISKDTSNQVFLKITSVDTRDTATYCCARRVSLTAYAMDYGOSTSVTVS 119

121 S 121
 120 S 120

RESULT 10

AA08107 standard; Protein: 139 AA.

AA08107;

25-JUL-1996 (first entry)

Murine anti-Protein C MAb HPC-4 VH gamma protein.

Epitope: activation; heavy chain; protein C; vitamin K; plasma protein;

zymogen; cleavage; mouse; humanised antibody; variable region;

light chain; inhibition; anticoagulant; coagulation; tumour.

Mus musculus.

Key Location/Qualifiers

Peptide 1..19 /note= "signal peptide"

Peptide 20..139 /note= "mature peptide"

MO0534652-A1.

21-DEC-1995.

09-JUN-1995; 95MO-US07372.

10-JUN-1994; 94US-0259321.

(OKLA-) OKLAHOMA MED RES FOUND.

Esmon CT, Rezaie A;

WPI: 1996-049681/05.

N-PSDB: AA09299.

Calcium-binding monoclonal antibody immunoreactive with Protein C -

inhibits Protein C anticoagulant activation by

thrombin-thrombomodulin, e.g. for treating tumours

Claim 2; Page 29; 41pp; English.

This is the amino acid sequence of the heavy chain variable region from

the murine anti-protein C monoclonal antibody HPC-4 which recognises

the activation peptide region (AA08106) of the heavy chain of protein

C, a vitamin K-dependent plasma protein zymogen. Protein C is converted

CC to activated protein C (APC) by cleavage between the Arg-Leu amino acid
 CC contained within the activation peptide sequence. HPC-4 prevents
 CC protein C activation to APC by binding to this region. The DNA sequences
 CC encoding the variable regions of the heavy and light chains of the
 CC antibody (AA09299-302) were used to construct humanised antibodies using
 CC the PCR primers AA09303-9. The humanised antibodies are useful as
 CC inhibitors of coagulation and can be used for the treatment of tumours by
 CC inhibiting the anticoagulant activity of APC by preventing conversion of
 CC protein C to APC.

XX Sequence 139 AA;

Query Match 82.5%; Score 522.5; DB 17; Length 139;
 Best Local Similarity 84.3%; Pred. No. 6.1e-44;
 Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILPSPQTLTSCSFGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 60

DB 20 QVTLKESGPGILPSPQTLTSCSFGSLSTSGMGVSWIRPQSGKLEMLAHYWDGDKR 79

QY 61 YNPGLKSRLLTISKDTSNQVFLKITSVDTRDTATYCCARRVSLTAYAMDYGOSTSVTVS 120
 DB 80 YNPGLKSRLLTISKDTSNQVFLKITSVDTRDTATYCCARRVSLTAYAMDYGOSTSVTVS 138

121 S 121
 139 S 139

RESULT 11

AA067655 standard; Protein: 139 AA.

AA067655;

21-AUG-1995 (first entry)

Mouse heavy chain variable region amino acid sequence.

Primer: PCR; amplify; kappa; light chain; variable region; mouse; human;

interleukin; antibody; hybridoma; CDR; framework; constant region;

heavy chain; disorder; antigenicity.

Synthetic.

Key Location/Qualifiers

Peptide 1..19 /label= signal peptide

Peptide 20..139 /label= mature peptide

WO9428159-A.

08-DEC-1994.

30-MAY-1994; 94WO-JP00859.

31-MAY-1993; 93JP-0129787.

(CHUS) CHUGAI SEIYAKU KK.

(CHUS) CHUGAI PHARM CO LTD.

Hirata Y, Sato K, Tsuchiya M;

WPI: 1995-022828/03.

N-PSDB: AA075889.

Antibody against IL-6 - useful for the therapy and treatment of

IL-6 related disorders.

Claim 10; Page 49; 82pp; Japanese.

The deduced amino acid sequence of the heavy chain variable region of

CC the mouse anti-human interleukin-6 (IL-6) antibody. The gene was
CC amplified by primers (AA075876-87) from cDNA derived from mRNA from
CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19
CC to produce plasmid pUC-SK2-Vh. The inserted fragment is used to
CC generate constructs (see AA075914-7) encoding fragments of an antibody to
CC the human IL-6 comprising (a) a light chain with (1) a variable region
CC containing 3 complementarity determining regions (CDR) (AA07201-3)
CC inserted into several framework regions (FR) (AA07204-7) and (11) a human
CC light chain constant region and (b) a heavy chain with (1) a variable
CC region containing 3 CDR (AA07212-4) inserted into an FR (AA07215-8) and
CC (11) a human light chain constant region. The FR of the light chain may
CC be mouse derived (AA075888) or from the human antibody FR1. The heavy
CC chain FR may also be mouse derived (AA075889) or from the human antibody
CC DAW. The antibodies can be used in the treatment of IL-6 related
CC disorders. The antibodies are useful as they have low antigenicity due to
CC the use of human derived sequences and low antigenicity mouse derived
CC sequences.

SO Sequence 139 AA:

Query Match Best Local Similarity 82.4%; Score 521.5; DB 16; Length 139;
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLSTLCFSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDGDKR 60
DB 20 QVTLKESGPGILQPSQTLSTLCFSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDGDKR 79
QY 61 YNPPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAY--AMDYWGQTSVT 118
DB 80 YNPPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAY--MEDYDEAMDYWGQTSVT 136
QY 119 VSS 121
DB 137 VSS 139

RESULT 12

ABG67188 standard: Protein; 121 AA.

AC ABG67188;
DT 24-SEP-2002 (first entry)

DE Human IgG1 antibody heavy chain variable region 15H4VH.

XX Hepatitis C virus vaccine; HCV; hypervariable region 1; HVRI;
XX envelope protein E2; antibody; helper T-lymphocyte; IgG1;
XX cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.

OS Homo sapiens.

PN WO200245743-A2.

PD 13-JUN-2002.

PE 07-DEC-2001; 2001WO-GB05421.

PF 09-DEC-2000; 2000GB-0030102.

PR 18-DEC-2000; 2000GB-0030789.

PA (ALLA/) ALLAIN J.

PI Allain J, Li C, Piccolella E;

PS WPI: 2002-508540/54.

XX Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T
XX lymphocytes and/or cytotoxic T lymphocytes able to bind to the
XX hypervariable 1 region of the infecting HCV strain
XX Example 4; Fig 2; 52pp; English.

XX The present invention relates to a hepatitis C virus (HCV) vaccine
CC comprising different groups of peptides each group being capable of
CC raising, in an infected individual, an antibody able to bind to the
CC hypervariable 1 (HVRI) region of the envelope protein E2 of the
CC infecting HCV strain. The different groups of peptides are
CC administered sequentially to raise antibodies, helper T-lymphocytes,
CC and cytotoxic T-lymphocytes which are cross-reactive to the HVRI
CC region of the infecting HCV. The vaccines are useful for preventing
CC and treating chronic HCV infections. ABG67186-ABG67189 represent
CC variable regions of human IgG1 antibody heavy chain.

SO Sequence 121 AA:

Query Match Best Local Similarity 82.1%; Score 520; DB 23; Length 121;
Matches 104; Conservative 7; Mismatches 7; Indels 4; Gaps 3;

QY 1 QVTLKESGPGILQPSQTLSTLCFSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDGDKR 59
DB 1 QVTLKESGPGILQPSQTLSTLCFSFGFSLSSTSGMGVSMIRPSGKGLMLAHYWDGDKR 60
QY 60 RYNPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAYAMDYWGQTSVT 119
DB 61 RYNPLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLAYAMDYWGQTSVT 117
QY 120 SS 121
DB 118 SS 119

RESULT 13

AAZ25396 standard: Protein; 121 AA.

AAZ25396;

DT 07-SEP-1999 (first entry)

DE WO9932630 Seq ID 35.

XX Paraquat; antibody; light chain; herbicide; resistant; crop plant;
XX weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;
XX free radical; lipid peroxidation; electron transport; photosystem II;
XX vacuole; cell surface; cytotoxic; sensitive.

OS Undefined.

PN WO9932630-A1.

PD 01-JUL-1999.

PE 15-DEC-1998; 98WO-GB03760.

PR 19-DEC-1997; 97GB-0026955.

PA (ZENEC) ZENEC LTD.

PI Holt DC, Jones PG;

PS WPI: 1999-405173/34.

XX Herbicide binding proteins and related polynucleotides

XX Disclosure: Page 43-44; 60pp; English.

XX This invention describes a novel herbicide binding protein which can
XX confer herbicide resistance activity. Crop plants, such as soybean,
XX cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,
XX potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,
XX barley, oat, turf grass, forage grass, sugar cane, pea, field bean,
XX rice, pine, poplar, apple, grape, citrus or nut plants, transformed
XX with a herbicide binding protein gene are resistant to the herbicide.

PR proteins, is derived from tobacco mosaic virus 54k protein and reacts
PR specifically with antibodies

PS Example 1; Page 7-8; 12pp; German.

XX This invention describes a novel polypeptide with tag sequence (I) or a
CC sequence derived from (I) by replacement of one or more amino acids (aa),
CC provided the three-dimensional/tertiary structure remains essentially
CC unchanged. The invention also describes (1) expression vector encoding a
CC fusion protein (FP) of a target polypeptide (II) and (I); (2) FP encoded
CC by the vector of (1); (3) antibodies (Ab), or their fragments, directed
CC against (I); and (4) kit containing the vector of (1) and optionally Ab.
CC (I) are used for isolation and/or detection of fusion polypeptides that
CC contain (I), by reaction with (I)-specific antibodies (Ab). Ab are used
CC for isolation, purification and/or detection of polypeptides (also for
CC determination of molecular weight, cell localization, post-translational
CC modification and interaction with other factors), and for diagnosis of
CC infection by tobacco mosaic virus (TMV). (I) is recognized by very
CC specific, high-affinity antibodies that do not cross-react significantly
CC with other cellular proteins (bacterial or eukaryotic). This sequence
CC represents the monoclonal antibody scFv54-1 which is used to illustrate
CC the method of the invention.

SQ Sequence 259 AA;

Query Match 81.5%; Score 516; DB 22; Length 259;

Best Local Similarity 81.8%; Pred. No. 5.6e-43;

Matches 99; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

OY	1	QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPSGKLEMLAHYWD	60
DB	3	QVTLKESGPGILQPSQTLSTLCFSFGSLSTSGMGVSWIROPSGKLEMLAHYWD	62
OY	61	YNPSLKSRLTISKDTSSNQVFLKITSVDTRPATYVCARVSLAYAMDYWGQGT	120
DB	63	YNPSLKSRLTISKDTSSNQVFLKITSVDTRPATYVCARVSLAYAMDYWGQGT	122
OY	121	S 121	
DB	123	S 123	

Search completed: July 9, 2003, 12:40:02
Job time : 71 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:40:08 ; Search time 22 Seconds

(without alignments)
640.309 Million cell updates/sec

Title: US-09-759-112A-7

Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSTL.....SLFAYAMDYMGCGTSVTVSS 121

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PC1_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/PC1US_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US60_NEM_PUB pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	100.0	121	9	US-09-759-112A-7
2	569	89.9	140	9	US-09-879-461-4
3	569	89.9	141	9	US-09-879-461-10
4	555	87.7	123	9	US-09-995-529-12
5	506.5	80.0	120	10	US-09-158-120A-32
6	506.5	80.0	143	10	US-09-881-823-8
7	502	79.3	141	9	US-09-879-461-12
8	499.5	78.9	120	9	US-10-011-931-3
9	470.5	74.3	126	9	US-10-265-713-4
10	470.5	74.3	126	10	US-09-764-304-4
11	470.5	74.3	141	9	US-10-265-713-2
12	470.5	74.3	141	10	US-09-764-304-2
13	468.5	74.0	120	10	US-09-771-415-2
14	468.5	74.0	120	10	US-09-796-848A-4
15	468.5	74.0	450	9	US-09-996-265-242
16	468.5	74.0	450	9	US-09-996-265-244
17	467.5	73.9	120	10	US-09-996-265-232
18	466.5	73.7	120	9	US-09-771-415-18
19	466.5	73.7	120	9	US-09-771-415-20

20	466.5	73.7	120	9	US-09-771-415-24	Sequence 24, Appl
21	466.5	73.7	120	9	US-09-771-415-26	Sequence 26, Appl
22	466.5	73.7	450	9	US-09-996-265-240	Sequence 210, App
23	466.5	73.7	450	9	US-09-996-265-240	Sequence 240, App
24	466.5	73.7	450	9	US-09-996-265-210	Sequence 210, App
25	466.5	73.7	450	9	US-09-996-265-240	Sequence 240, App
26	465.5	73.5	450	9	US-09-996-265-242	Sequence 242, App
27	465.5	73.5	450	9	US-09-996-265-242	Sequence 242, App
28	465.5	73.5	450	9	US-09-996-265-246	Sequence 246, App
29	465.5	73.5	450	9	US-09-996-265-246	Sequence 246, App
30	465.5	73.5	450	9	US-09-996-265-232	Sequence 232, App
31	465.5	73.5	450	9	US-09-996-265-242	Sequence 242, App
32	465.5	73.5	450	9	US-09-996-265-244	Sequence 244, App
33	465.5	73.5	450	9	US-09-996-265-246	Sequence 246, App
34	464.5	73.4	120	9	US-09-771-415-22	Sequence 22, Appl
35	463.5	73.2	450	9	US-09-996-265-248	Sequence 248, App
36	463.5	73.2	450	9	US-09-996-265-248	Sequence 248, App
37	462.5	73.1	120	9	US-09-996-265-7	Sequence 7, Appl
38	462.5	73.1	120	9	US-09-996-265-7	Sequence 7, Appl
39	462.5	73.1	120	10	US-09-796-848A-2	Sequence 2, Appl
40	462.5	73.1	450	9	US-10-135-636-1	Sequence 1, Appl
41	461.5	72.9	450	9	US-09-996-268-232	Sequence 232, App
42	461.5	72.9	450	9	US-09-996-268-234	Sequence 234, App
43	461.5	72.9	450	9	US-09-996-268-236	Sequence 236, App
44	461.5	72.9	450	9	US-09-996-265-232	Sequence 232, App
45	461.5	72.9	450	9	US-09-996-265-234	Sequence 234, App

ALIGNMENTS

RESULT 1
US-09-759-112A-7
; Sequence 7, Application US/09759112A
; Publication No. US20030100741A1
GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LI
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOYPIC ANTIBODY REACTI
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759, 112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mouse
US-09-759-112A-7

Query Match 100.0%; Score 633; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGKGVSMIRPSCGGLGMLAHYWDKKR 60
|||||
DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGKGVSMIRPSCGGLGMLAHYWDKKR 60
|||||
QY 61 YNPSLKSRLTSSKDPSSNQVFLKITSVDTROTATYTCARRVSLFAYAMDYMGCGTSVTVSS 120
|||||
DB 61 YNPSLKSRLTSSKDPSSNQVFLKITSVDTROTATYTCARRVSLFAYAMDYMGCGTSVTVSS 120
|||||
QY 121 S 121
|
DB 121 S 121

RESULT 2
US-09-879-461-4
; Sequence 4, Application US/09879461
; Publication No. US20020193575A1

GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
ZIP: 19406-2799
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIORITY DATA:
PRIORITY NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-879-461-4

Query Match 89.9%; Score 569; DB 9; Length 140;
Best Local Similarity 90.1%; Pred. No. 6.1e-43;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 1 QVTLKESGPGIILPQSQTLSITCSFSGFSLSTSGMGVSWIRPSGKGLEMLAHIMYDDDKR 60
|||||
QY 61 YNPSLSRLTISKDTSSNOVFLKITSVDFTATYTCARVSLTAYAMDYWGCGSTVTS 120
|||||
Db 80 YNPSLSRLTISKDTSSNOVFLKITSVDFTATYTCARRETVFYWFYWGAGTIVTS 139
|||||

QY 121 S 121
|
Db 140 S 140

RESULT 3
US-09-879-461-10
Sequence 10, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
ZIP: 19406-2799
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIORITY DATA:
PRIORITY NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-879-461-10

Query Match 89.9%; Score 569; DB 9; Length 141;
Best Local Similarity 90.1%; Pred. No. 6.1e-43;
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 1 QVTLKESGPGIILPQSQTLSITCSFSGFSLSTSGMGVSWIRPSGKGLEMLAHIMYDDDKR 60
|||||
QY 21 QVTLKESGPGIILPQSQTLSITCSFSGFSLSTSGMGVSWIRPSGKGLEMLAHIMYDDDKR 80
|||||
Db 61 YNPSLSRLTISKDTSSNOVFLKITSVDFTATYTCARVSLTAYAMDYWGCGSTVTS 120
|||||
QY 81 YNPSLSRLTISKDTSSNOVFLKITSVDFTATYTCARRETVFYWFYWGAGTIVTS 140
|||||

QY 121 S 121
|
Db 141 S 141

RESULT 4
US-09-995-529-12
Sequence 12, Application US/09995529
Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
Huse, William D.
Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 123
LENGTH: 123
TYPE: PRT

QY 1 QVTLKESGPEILQPSQTLSTLCTCSFGSGSLSTSGMGVSNIRQPSCKGLEMLAHYINDDKR 600
||:|||||:|||||:|||||:|||||:|||||
Dp 1 QVELQESGPEILQPSQTLSTLCTCSFGSGSLSTSGMGVSNIRQPSCKGLEMLADINDDKD 600

CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutcon, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-879-461-12

Query Match 79.3% Score 502; DB 9; Length 141;
Best Local Similarity 76.9%; Pred. No. 4.7e-37;
Matches 93; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGKGLLEMLAHYWDKDR 60
DB 21 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGKGLLEMLAHYWDKDR 80
QY 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAAYMDYWGOSTSVTVS 120
DB 81 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAAYMDYWGOSTSVTVS 140
QY 121 S 121
DB 141 S 141

RESULT 8

US-10-011-931-3
Sequence 3, Application US/10011931.
Publication No. US20030026806A1

GENERAL INFORMATION:

APPLICANT: WITTE, ALISON
APPLICANT: VARNUM, BRIAN C.
APPLICANT: OZAN, ZUEMING
APPLICANT: VEZINA, CHRIS
TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
FILE REFERENCE: A-731
CURRENT APPLICATION NUMBER: US/10/011,931
CURRENT FILING DATE: 2002-04-01
PRIORITY APPLICATION NUMBER: US 60/244,118
PRIORITY FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 120
TYPE: PRT
ORGANISM: Mus musculus
US-10-011-931-3

Query Match 78.9% Score 499.5; DB 9; Length 120;
Best Local Similarity 81.0%; Pred. No. 6.6e-37;
Matches 98; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGKGLLEMLAHYWDKDR 60
DB 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGKGLLEMLAHYWDKDR 60
QY 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAAYMDYWGOSTSVTVS 120
DB 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAAYMDYWGOSTSVTVS 119
QY 121 S 121
DB 120 S 120

RESULT 9

US-10-265-713-4
Sequence 4, Application US/10265713
Publication No. US20030095964A1

GENERAL INFORMATION:

APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KURAMA, YOSHIOHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIORITY APPLICATION NUMBER: US/09/225,322
PRIORITY FILING DATE: 1999-01-05/08/454,680
PRIORITY APPLICATION NUMBER: US 08/408,133
PRIORITY FILING DATE: 1995-05-31
PRIORITY APPLICATION NUMBER: US 08/292,178
PRIORITY FILING DATE: 1992-09-17
PRIORITY APPLICATION NUMBER: JP 3-238375
PRIORITY FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 126
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-265-713-4

Query Match 74.3% Score 470.5; DB 9; Length 126;
Best Local Similarity 75.4%; Pred. No. 2.4e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGKGLLEMLAHYWDKDR 60
DB 5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGKGLLEMLAHYWDKDR 64
QY 61 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAAYMDYWGOSTSVTVS 119
DB 65 YNPSLKRRLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAAYMDYWGOSTSVTVS 124
QY 120 SS 121
DB 125 SS 126

RESULT 10

US-09-764-304-4
Sequence 4, Application US/09764304
Patent No. US20020026036A1

GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: HANAI, NOBUO

APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 126
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Rat hybridoma
US-09-764-304-4

Query Match 74.3%; Score 470.5; DB 10; Length 126;
Best Local Similarity 75.4%; Pred. No. 2,4e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWTRQPSGKLEWLAHIYDDDKR 60
|||||
5 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWTRQPSGKLEWLAHIYDDDKR 64
|||||
QY 61 YNPSLKSRLTISKDSSNQVFLKITSVDTRDTATFYCCARRVSLTA-YAMDYWGQGSTVTV 119
|||||
DB 65 YNPSLKNRLTISKDSSNQVFLKITSVDTRDTATFYCCARRVSLTA-YAMDYWGQGSTVTV 124
|||||
QY 120 SS 121
||
DB 125 SS 126

RESULT 11

US-10-265-713-2
Sequence 2, Application US/10265713
Publication No. US20030095964A1
GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 141
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-265-713-2

Query Match 74.3%; Score 470.5; DB 9; Length 141;
Best Local Similarity 75.4%; Pred. No. 2.7e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWTRQPSGKLEWLAHIYDDDKR 60
|||||
DB 20 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWTRQPSGKLEWLAHIYDDDKR 79
|||||
QY 61 YNPSLKSRLTISKDSSNQVFLKITSVDTRDTATFYCCARRVSLTA-YAMDYWGQGSTVTV 119
|||||
DB 80 YNPSLKNRLTISKDSSNQVFLKITSVDTRDTATFYCCARRVSLTA-YAMDYWGQGSTVTV 139
|||||
QY 120 SS 121
||
DB 140 SS 141

RESULT 12

US-09-764-304-2
Sequence 2, Application US/09764304
Patent No. US20020026036A1
GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 141
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Rat hybridoma
US-09-764-304-2

Query Match 74.3%; Score 470.5; DB 10; Length 141;
Best Local Similarity 75.4%; Pred. No. 2.7e-34;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWTRQPSGKLEWLAHIYDDDKR 60
|||||
DB 20 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWTRQPSGKLEWLAHIYDDDKR 79
|||||
QY 61 YNPSLKSRLTISKDSSNQVFLKITSVDTRDTATFYCCARRVSLTA-YAMDYWGQGSTVTV 119
|||||
DB 80 YNPSLKNRLTISKDSSNQVFLKITSVDTRDTATFYCCARRVSLTA-YAMDYWGQGSTVTV 139
|||||

QY 120 SS 121
Db 140 SS 141

RESULT 13

US-09-771-415-2
Sequence 2, Application US/09771415
Patent No. US20020164326A1
GENERAL INFORMATION:
APPLICANT: Young, James F.
APPLICANT: Koenig, Scott
APPLICANT: Johnson, Leslie S.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: ultra high affinity Neutralizing Antibodies
FILE REFERENCE: 469201-520
CURRENT APPLICATION NUMBER: US/09/771,415
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,426
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mouse human
OTHER INFORMATION: chimeric antibody heavy chain variable chain
US-09-771-415-2

Query Match 74.0%; Score 468.5; DB 9; Length 120;
Best Local Similarity 72.7%; Pred. No. 3.5e-34;
Matches 88; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
Db 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYGOSTSVTS 120
Db 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYGOSTSVTS 120
QY 121 S 121
Db 120 S 120

RESULT 14

US-09-796-848A-4
Sequence 4, Application US/09796848A
Patent No. US20020098189A1
GENERAL INFORMATION:
APPLICANT: Young, James F.
APPLICANT: Johnson, Leslie S.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
Producing Them
FILE REFERENCE: 469201-526
CURRENT APPLICATION NUMBER: US/09/796,848A
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 120
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain
OTHER INFORMATION: variable region sequence of a humanized antibody.
US-09-796-848A-4

Query Match 74.0%; Score 468.5; DB 10; Length 120;
Best Local Similarity 72.7%; Pred. No. 3.5e-34;
Matches 88; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
Db 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYGOSTSVTS 120
Db 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYGOSTSVTS 120
QY 121 S 121
Db 120 S 120

RESULT 15

US-09-996-288-208
Sequence 208, Application US/09996288
Patent No. US20020177126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophyl
and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 208
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-208

Query Match 74.0%; Score 468.5; DB 9; Length 450;
Best Local Similarity 72.7%; Pred. No. 1.4e-33;
Matches 88; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
Db 1 QVTLKESGPGILQPSQTLSTGSGFSLSTSGMGVSWIRPGSGKLEMLAHYWDKDR 60
QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYGOSTSVTS 120
Db 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYCARVSLTAYAMDYGOSTSVTS 120
QY 121 S 121
Db 120 S 120

Search completed: July 9, 2003, 12:43:48
Job time: 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:37:27 ; Search time 39 Seconds

(without alignments)
298.263 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTL.....SLRAYANDYWGQSTVSS 121

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551.5	87.1	122	2 S11740	Ig heavy chain pre
2	543.5	85.9	107	2 PT0174	Ig heavy chain pre
3	491	77.6	107	2 A49442	Ig heavy chain V r
4	474.5	75.0	113	2 S26465	Ig heavy chain V r
5	472.5	74.6	116	2 S26328	Ig heavy chain V r
6	471	74.4	138	2 S31513	Ig heavy chain - h
7	460	72.7	121	2 S09959	Ig heavy chain V r
8	454.5	71.8	124	2 A49002	Ig heavy chain V r
9	448	70.8	103	2 B25913	Ig heavy chain pre
10	436	68.9	374	2 S69339	Ig heavy chain V r
11	419.5	66.3	120	1 GIHDCO	Ig heavy chain V-I
12	412	65.1	121	2 A30005	Ig heavy chain V r
13	410	64.8	119	2 S18555	Ig heavy chain V r
14	407	64.3	125	1 MHHMWC	Ig heavy chain V-I
15	402.5	63.6	147	1 G2HDCS	Ig heavy chain pre
16	395	62.4	121	1 GIHDCO	Ig heavy chain V-I
17	390.5	61.7	122	2 S20809	Ig heavy chain V r
18	384.5	60.7	120	2 PL0087	Ig heavy chain V r
19	384	60.7	144	1 G2MS14	Ig heavy chain V r
20	383.5	60.6	118	2 S18556	Ig heavy chain pre
21	382	60.3	146	2 S09711	Ig heavy chain V r
22	379.5	60.0	117	2 S38563	Ig heavy chain V r
23	377	59.6	96	2 S26924	Ig heavy chain V r
24	377	59.6	140	2 I37782	Ig variable region
25	376	59.4	147	2 S13519	Ig heavy chain V r
26	373.5	59.0	122	2 A49049	Ig heavy chain V r
27	373.5	59.0	137	2 S31676	Ig heavy chain V r
28	372	58.8	135	2 S31511	Ig heavy chain - h
29	371	58.6	96	2 S26923	Ig heavy chain V r

30	371	58.6	109	2 PH1023	Ig heavy chain V r
31	371	58.6	119	1 GIHDCO	Ig heavy chain V-I
32	371	58.6	140	2 S55028	Ig heavy chain V r
33	370.5	58.5	130	2 S30534	Ig heavy chain V r
34	370	58.5	155	2 S31512	Ig heavy chain - h
35	369	58.3	130	2 S31690	Ig heavy chain V r
36	368.5	58.2	139	2 A32456	Ig heavy chain pre
37	368.5	58.2	141	2 S52446	Ig heavy chain V r
38	368	58.1	117	2 I57810	gene C72-3A1 prote
39	366	57.8	111	2 S26324	Ig heavy chain V r
40	363	57.3	149	2 S30752	Ig heavy chain pre
41	362	57.2	128	2 S31514	Ig heavy chain - h
42	360.5	57.0	129	2 S44114	Ig heavy chain V r
43	360	56.9	127	2 S19668	Ig heavy chain V r
44	360	56.9	135	2 S78051	Ig heavy chain pre
45	359.5	56.8	139	2 S31586	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S11740

Ig heavy chain precursor V-D-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S11740

R:Hayakawa, K.; Carmack, C.E.; Hyman, R.; Hardy, R.R.

A:Submitted to the EMBL Data Library, May 1990

A:Description: Natural autoantibodies to thymocytes: Origin, VH genes, fine specifici

A:Reference number: S11740

A:Accession: S11740

A:Molecule type: mRNA

A:Residues: 1-122 <EMBL>

A:Cross-references: EMBL:X53097; NID:952368; PIDN:CA37261.1; PID:9762983

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:22-106/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 91.4%; Score 551.5; DB 2; Length 122;

Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Qy

1 QVTLKESGPGILQPSQTLSCFSFGSLSGMGVSIROPKGLAHYWDKDKR 60

8 QVTLKESGPGILQPSQTLSCFSFGSLSGMGVSIROPKGLAHYWDKDKR 67

Qy

61 YNPSIKSRLTISKDTSNQVFLKITSVDTRDPATYVCARRVSLRAYANDYWGQSTS 116

68 YNPSIKSRLTISKDTSNQVFLKITSVDTRDPATYVCARRVSLRAYANDYWGQSTS 122

RESULT 2

PT0174

Ig heavy chain precursor V region (IdB5.7) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996

C:Accession: PT0174

R:Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.

Mol. Immunol. 28, 505-515, 1991

A:Title: Specificity and variable region cDNA sequence of an isogenic monoclonal ant

A:Reference number: PT0174; MUID:91287738; PMID:1712074

A:Accession: PT0174

A:Molecule type: mRNA

A:Residues: 1-143 <PER>

A:Experimental source: strain BALB/c

C:Comment: IdB5.7 is an antibody to anti-alpha (1-6) dextran.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-118/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.9%; Score 543.5; DB 2; Length 143;

Matches 85.9%; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

S09959
 Ig heavy chain V region (31-9D) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
 C:Accession: S09959
 R:Reininger, L., Shibata, T., Ozaki, S., Shirai, T., Jaton, J.C., Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A:Reference number: S09955; MUID:90269328; PMID:2347362
 A:Accession: S09959
 A:Molecule type: mRNA
 A:Residues: 1-121 <RET>
 A:Cross-references: EMBL:X51847; NID:G55247; PIDN:CA036140.1; PID:9930215
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 8
A49002 -
Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49002
R:Stuber, F.; Lee, S. K.; Bridges Jr., S. L.; Koopman, W. J.; Schroeder, H. W. J.; Gaaklin, F.
Arthritis Rheum. 35, 900-904, 1992
A:Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II genes
A:Reference number: A49002; MUID:92352481; PMID:1322670
A:Accession: A49002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-124 <STU>
C:Cross-references: GB:M90808; NID:g185515; PIDN:AAA52989.1; PID:g567176
C:Experimental source: EBV-transformed lymphoblastoid cell line SSH23
A:Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIPI:110262)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match	71.8%;	Score 454.5;	DB 2;	Length 124;
Best Local Similarity	70.2%;	Pred. No. 5.1e-36;		
Matches 87;	Conservative 16;	Mismatches 18;	Indels 3;	Gaps 2

Qy	1	OVLKSSGGIILOPQOTLILTCFSFGFSLSTGCMGVSIRPQSGKGLLEMLAHYWDGDR	60
	1	QITLKESGPIVLRPQTFLTCTFSGFSLSTGCVGMIRQPPKALEMLALLIYMDRR	60
Db			
Qy	61	YNSLTKSLTISMDSSNOVELKITRSPDPRATAYYCAR-RVSLFLAY--ANDYWGQCTSY	117
Db	61	YSSLSLKRLLITIKDTSKNQVLTMTNMDVDTAIIYCAHMTVDSSGIIILGFDYWGQSTLV	120
Qy			
	118	TVSS	121
Db	121	TVSS	124

RESULT 9

B25913
Ig heavy chain precursor V region (BFL23) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
C:Accession: B25913
R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A:Reference number: A94148; MUID:87175692; PMID:3104915
A:Accession: B25913
A:Molecule type: DNA
A:Residues: 1-103 <LAW>
A:Note: The authors translated the codon TGT for residue 11 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:19-103/Domain: immunoglobulin homology <IMM>

Query Match	70.8%	Score 448	DB 2	Length 103
Best Local Similarity	85.9%	Pred. No. 1.7e-35		
Matches	85	Conservative	4	Mismatches 10
				Indels 0
				Gaps 0

OY	1	QVTLKESPGILLOSOTLTLCSFGSGFLSTSGMGVSIROP	SGKLEMLHIYWD	DDKR	60
					:
Db	5	QVTLKEGPGILPOSOTLTLCSFGSGFLSTSGMGVSIROP	SGKLEMLHI	LLND	SKY 64
OY	61	YNPSLKSRLTISKDTSNQVFLKITSVPT	RDATATY	YCAR	99
		:	:		
Db	65	YNPAKLSRLTISKDTYNNQVFLKLANDVT	ADATATY	YCAR	103

RESULT 10
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogné, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease
A:Reference number: S69339; PMID:95262687; PMID:7744049
A:Accession: S69339
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match	68.9%;	Score 436;	DB 2;	Length 374;
Best Local Similarity	66.4%;	Pred. No. 9.9e-34;		
Matches	83;	Conservative 17;	Mismatches 19;	Indels 6;
				Gaps 2;

[illegible]

RESULT 11

[illegible]

QY	QZ
1 QVTLKESPGILOPSQITSLTCSFGSGFSLTSCGMGVSMIRQPSCKGLEWLAHIYWDDDR 60	1 QVTLKESPGILOPSQITSLTCSFGSGFSLTSCGMGVSMIRQPSCKGLEWLAHIYWDDDR 60
1 QITLKESPTLPTETITLTTCFFSGFSLTSCGVGVMTQRQRPCKALELAFINWDDNR 60	1 QITLKESPTLPTETITLTTCFFSGFSLTSCGVGVMTQRQRPCKALELAFINWDDNR 60

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:24:47 ; Search time 23 seconds

(without alignments)
218.202 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSTL.....SLTAVAMDYWGQTSVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	419.5	66.3	120	1	HY2B_HUMAN
2	407	64.3	125	1	HY2D_HUMAN
3	402.5	63.6	147	1	HY2H_HUMAN
4	395	62.4	121	1	HY2E_HUMAN
5	384	60.7	144	1	HY43_MOUSE
6	371	58.6	119	1	HY2C_HUMAN
7	358.5	56.6	126	1	HY2A_HUMAN
8	353	55.8	137	1	HY46_MOUSE
9	327	51.7	115	1	HY44_MOUSE
10	317	50.1	129	1	HY2E_HUMAN
11	315.5	49.8	135	1	HY02_XENLA
12	312.5	49.4	116	1	HY60_MOUSE
13	309.5	48.9	146	1	HY2I_HUMAN
14	306.5	48.4	126	1	HY3K_HUMAN
15	305	48.2	117	1	HY2G_HUMAN
16	302	47.7	121	1	HY3J_HUMAN
17	299.5	47.3	116	1	HY61_MOUSE
18	299.5	47.3	122	1	HY3G_HUMAN
19	299.5	47.3	136	1	HY16_MOUSE
20	298	46.3	113	1	HY47_MOUSE
21	293	46.3	116	1	HY45_MOUSE
22	288	45.5	117	1	HY62_MOUSE
23	287.5	45.4	122	1	HY3H_HUMAN
24	287	45.3	136	1	HY01_XENLA
25	278.5	44.0	119	1	HY40_MOUSE
26	278	43.9	119	1	HY3I_HUMAN
27	275.5	43.5	119	1	HY37_MOUSE
28	273	43.1	117	1	HY41_MOUSE
29	272.5	43.0	119	1	HY38_MOUSE
30	271.5	42.9	116	1	HY3I_HUMAN
31	271	42.8	117	1	HY42_MOUSE
32	266	42.0	119	1	HY3L_HUMAN
33	262.5	41.5	114	1	HY3B_HUMAN

34	262.5	41.5	119	1	HY3M_HUMAN
35	261	41.2	115	1	HY3D_HUMAN
36	261	41.2	115	1	HY3E_HUMAN
37	260.5	41.2	118	1	HY3V_HUMAN
38	259.5	41.0	122	1	HY20_MOUSE
39	256.5	40.5	119	1	HY3N_HUMAN
40	256	40.4	118	1	HY39_MOUSE
41	256	40.4	123	1	HY24_MOUSE
42	256	40.4	142	1	HY01_RAT
43	255	40.3	123	1	HY23_MOUSE
44	255	40.3	123	1	HY25_MOUSE
45	254.5	40.2	115	1	HY3S_HUMAN

ALIGNMENTS

RESULT 1					
HY2B_HUMAN					
ID	HY2B_HUMAN	STANDARD:	PRT:	120 AA.	
AC	P01815:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V-II region COR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
ON	(1)				
RP	SEQUENCE.				
RX	MEDLINE=70258837; PubMed=5449120;				
RA	Press E.M., Hogg N.M.;				
RT	"The amino acid sequences of the Pd fragments of two human gamma-1				
RT	heavy chains."				
RL	Biochem. J. 117:641-660(1970).				
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA				
CC	PROTEIN.				
DR	PIR: A02089; GIHUCO.				
DR	HSP; P01825; 7FAB.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003596; Ig_V.				
DR	Pfam: PF00047; Ig_1.				
DR	SMART: SM00406; IgV_1.				
KW	Immunoglobulin V region; Glycoprotein.				
FT	MOD_RES 1				
FT	DISULFID 22				
FT	CARBOHYD 62				
FT	NON_TER 120				
SO	SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;				
Query Match	66.3%; Score 419.5; DB 1; Length 120;				
Best Local Similarity	68.3%; Pred. No. 1,6e-35;				
Matches	84; Conservative 15; Mismatches 19; Indels 5; Gaps 2;				
OY	1 QVTLKESGPGILQPSQTLSTLSTGSGFSTSGMGVSWTROPKGLKLEMLAHYWDDDR 60				
DB	1 QVTLKESGPGILQPSQTLSTLSTGSGFSTSGMGVSWTROPKGLKLEMLAHYWDDDR 60				
OY	61 YNPSEKRLTKISDKSSNOVFLKITSVDTRDTATYYCARVSLTAV--MDYWGQTSVT 118				
DB	61 YNPSEKRLTKISDKSSNOVFLKITSVDTRDTATYYCARVSLTAV--MDYWGQTSVT 118				
OY	119 VSS 121				
DB	118 VSS 120				
RESULT 2					
HY2D_HUMAN					
ID	HY2D_HUMAN	STANDARD:	PRT:	125 AA.	
AC	P01817:				
DT	21-JUL-1986 (Rel. 01, Created)				

21-JUL-1986 (Rel. 01, last sequence update)
15-JUL-1999 (Rel. 38, last annotation update)
Ig heavy chain V-II region MCE.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
SEQUENCE.
MEDLINE=81118242; PubMed=6780622;
Gaber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
Litman G.W.;
"Molecular basis for the temperature-dependent insolubility of
cryoglobulins. X. The amino acid sequence of the heavy chain variable
region of MCE."
J. Immunol. 126:1212-1216(1981).
-1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
CRYOGLOBULIN.
CC PIR: A02092; MHDMC.
DR HSP: P01825; 7RAB.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT NON_TER 1
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADFC40F47B55 CRC64;
Query Match 64.3%; Score 407; DB 1; Length 125;
Best Local Similarity 62.3%; Pred. No. 3e-34;
Matches 79; Conservative 17; Mismatches 25; Indels 4; Gaps 1;
QY 1 QVTLKESGPGIILPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDKDKR 60
D 1 QVTLKESGPGIILPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDKDKR 60
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR---RVSITAYAMDYGQCTS 116
D 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR---RVSITAYAMDYGQCTS 116
QY 117 VTWSS 121
D 117 VTWSS 125
Db 121 VTWSS 125
RESULT 3
HV2H_HUMAN STANDARD; PRT; 147 AA.
P04438;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, last sequence update)
15-JUL-1999 (Rel. 38, last annotation update)
Ig heavy chain V-II region SSS precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=84298107; PubMed=6089186;
Takahashi N., Noma T., Honjo T.;
"Rearranged immunoglobulin heavy chain variable region (VH)
pseudogene that deletes the second complementarity-determining
region."
Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR PIR: A02090; G2HUCS.
DR HSP: P01825; 7RAB.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SSS.
FT DOMAIN 20 118 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16323 MW; FCBDCB3D00F6B666 CRC64;
Query Match 63.6%; Score 402.5; DB 1; Length 147;
Best Local Similarity 62.3%; Pred. No. 1e-33;
Matches 76; Conservative 16; Mismatches 23; Indels 7; Gaps 1;
QY 1 QVTLKESGPGIILPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDKDKR 60
D 20 QVTLKESGPGIILPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDKDKR 60
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR-----RVSITAYAMDYGQ 113
D 80 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR-----RVSITAYAMDYGQ 113
QY 114 GT 115
D 140 GT 141
Db 140 GT 141
RESULT 4
HV2H_HUMAN STANDARD; PRT; 121 AA.
P01818;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, last sequence update)
15-JUL-1999 (Rel. 38, last annotation update)
Ig heavy chain V-II region HE.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
SEQUENCE.
MEDLINE=70114712; PubMed=5264153;
Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
"Subgroups of amino acid sequences in the variable regions of
immunoglobulin heavy chains."
Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
-1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN.
CC PIR: A02093; G1HJHE.
DR HSP: P01825; 7RAB.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;
Query Match 62.4%; Score 395; DB 1; Length 121;
Best Local Similarity 61.5%; Pred. No. 4.6e-33;
Matches 75; Conservative 20; Mismatches 25; Indels 2; Gaps 2;
QY 1 QVTLKESGPGIILPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDKDKR 59
D 1 QVTLKESGPGIILPSQTLSTLCSFSGFSLSTSGMGVSWIRPQSGKLEMLAHYWDKDKR 60
QY 60 RYNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARVSLTAYAMDYGQSVYV 119
D 61 RYNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARVSLTAYAMDYGQSVYV 119
QY 120 SS 121
D 120 SS 121
Db 120 SS 121


```

RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.W.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RL heavy chains."
RL Blochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
CC SEED OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
DR PIR: A02091; G1HDM.
DR HSSP; P01789; IMCP.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT NON_TER 119
FT SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;
SQ
Query Match 58.6%; Score 371; DB 1; Length 119;
Best Local Similarity 61.3%; Pred. No. 1,2e-30;
Matches 76; Conservative 15; Mismatches 25; Indels 8; Gaps 3
QY 1 QVTLKESGPGLILOSQTLSLCSFSGFSLSGSGVSMIROPSGKLEMLHIYWD---D 57
DB 1 QVTLRESGPALVRPQTQLTLCTFSGFSLSGETMCMVAMIRQPPGALBMLA---WDI 57
QY 58 DKRRNPSTLSKSLTISKTRSSNOVFLKITSVTRDTATYYCARARVSLTAYADYWGQGRSV 117
DB 58 DKRYGASLETRLAVSKDTSKNQVYLSMNTVGPGRATYYCAR--SCGSQYEDYWGQGLV 115
QY 118 TVSS 121
DB 111
DB 116 TVSS 119
RESULT 7
HY2A_HUMAN STANDARD; PRT; 126 AA.
ID HY2A_HUMAN
AC P01814;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74005511; PubMed=4742735;
RA Putnam F.W., Florent G., Paul C., Shindou T., Shintzu A.;
RT "Complete amino acid sequence of the mu heavy chain of a human Igm
RL immunoglobulin."
RL Science 182:287-291(1973).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR: A02088; MHHOU.
DR HSSP; P01825; 7FAB.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT DISULFD 22
FT NON_TER 97
FT SEQUENCE 126 AA; 14276 MW; A85C0BED0ABC296F CRC64;
SQ
Query Match 56.6%; Score 358.5; DB 1; Length 126;
Best Local Similarity 60.3%; Pred. No. 2.3e-29;
Matches 76; Conservative 19; Mismatches 26; Indels 5; Gaps 2;

```

```

QY 1 QVTLKESGPGILPSPQTLSTLCSFSGSLTSGMGVSMIRPSPGKLEMLAHYWDKDR 60
DB 1 QVTLKESGPGILPSPQTLSTLCSFSGSLTSGMRVSMIRPSPGKLEMLAHYWDKDR 60
QY 61 YNPISLRITLSTKSDTSNOVFLKITSVDTRDTATYCARV-SLTA----YANDYWGCGT 115
DB 61 WSTSLRITLSTKSDTSNOVFLKITSVDTRDTATYCARVSYMAGYVYMDVWGCGT 120
QY 116 SYTVSS 121
DB 121 TVTVSS 126

RESULT 8
HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP MEDLINE-89238351; PubMed-2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
gene segment."
RL Mol. Immunol. 26:431-434(1989).
RN [2]
RP MEDLINE-78094475; PubMed-414225;
RA Jilke R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
immunoglobulin heavy chain."
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN [3]
RP MEDLINE-79148758; PubMed-428562;
RA Schechter I., Wolf O., Zemel R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors."
RL Fed. Proc. 38:1839-1845(1979).
RN [4]
RP MEDLINE-74170779; PubMed-4524622;
RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
RT "Amino acid sequence of the variable region of the heavy (alpha)
chain of a mouse myeloma protein with anti-hapten activity."
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN [5]
RP MEDLINE-77244979; PubMed-268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RT "Unpublished results, cited by:
Polian E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
```

```

DR PIR; P0102; AVMS35.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
KW Immunoglobulin V region; signal.
FT SIGNAL 1
FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 137 FRAMEWORK-4.
FT DISULFID 40 114 BY SIMILARITY.
FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).
FT CONFLICT 15 15 G -> H (IN REF. 2).
FT CONFLICT 77 78 G -> YG (IN REF. 4).
FT CONFLICT 102 102 N -> D (IN REF. 4).
FT CONFLICT 123 123 MISSING (IN REF. 4).
FT NON_TER 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 55.8%; Score 353; DB 1; Length 137;
Best Local Similarity 59.2%; Pred. No. 9e-29;
Matches 71; Conservative 19; Mismatches 28; Indels 2; Gaps 2;

QY 2 VTLKESGPGILPSPQTLSTLCSFSGSLTSGMGVSMIRPSPGKLEMLAHYWDKDR 61
DB 20 VOLQESGPGILPSPQTLSTLCSFSGSLTSGMRVSMIRPSPGKLEMLAHYWDKDR 78
QY 62 NPSLKRITLSTKSDTSNOVFLKITSVDTRDTATYCARVSLTAANDYWGCGTSYVSS 121
DB 79 NPSLKRITLSTKSDTSNOVFLKITSVDTRDTATYCARVSLTAANDYWGCGTSYVSS 137

RESULT 9
HV44_MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region P14 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP MEDLINE-81012133; PubMed-674258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
```

KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19 IG HEAVY CHAIN V REGION PJ14.
 FT CHAIN 20 115
 FT NON_TER 115 115
 SO SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
 Query Match 51.7%; Score 327; DB 1; Length 115;
 Best Local Similarity 64.3%; Pred. No. 3,1e-26;
 Matches 63; Conservative 14; Mismatches 19; Indels 2; Gaps 1;
 QY 1 QVTLKESGPGILQPSQTLSTLCTSGFSLSTSGMGVSIKROPSGKGLMIAHYWDDDKR 60
 DB 20 QVQKESGPGILVAPSSQSLTCTVSGFSL--TGXGVNVRQPPGKGLMIGMIDGSTD 77
 QY 61 YNPSLKSRITSKDTSNNOVFLKITSVDTRDTATYTCARVSLAY-----AMDYWG 112
 DB 61 YNPSLRGRVITISVDTSRNOQSLNLRSMGADTATYTCARGNPPYDYGTSDDGIDVWG 120
 QY 113 QGTSVTYSS 121
 DB 121 QGTIVHVS 129
 RESULT 11
 HV02_XENLA STANDARD; PRT; 135 AA.
 AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)

RESULT 10
 ID 2F_HUMAN STANDARD; PRT; 129 AA.
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region WHH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN RP SEQUENCE.
 RX MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Tetsu D., Debilire B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 PROTEIN.
 CC PIR: A02059; D2HWA.
 DR HSSP; P01825; 7FAB.
 DR GlycoSiteDB; P01824;
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv_1.
 DR Immunoglobulin V region.
 NON_TER 129 129
 SO SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
 Query Match 50.1%; Score 317; DB 1; Length 129;
 Best Local Similarity 49.6%; Pred. No. 3,3e-25;
 Matches 64; Conservative 18; Mismatches 39; Indels 8; Gaps 1;
 QY 1 QVTLKESGPGILQPSQTLSTLCTSGFSLSTSGMGVSIKROPSGKGLMIAHYWDDDKR 60
 DB 1 RLQDQESGPGILVAPSSQSLTCTVSGFSLTGYWIRPPGKGLMIGCVITYGSIY 60
 QY 61 YNPSLKSRITSKDTSNNOVFLKITSVDTRDTATYTCARVSLAY-----AMDYWG 112
 DB 61 YNPSLRGRVITISVDTSRNOQSLNLRSMGADTATYTCARGNPPYDYGTSDDGIDVWG 120
 QY 113 QGTSVTYSS 121
 DB 121 QGTIVHVS 129

DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region XIG14 precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 [1]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=88176921; PubMed=2451244;
 RA Schwaeger J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
 from cDNA sequence: implications for evolution of immunoglobulin
 domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; J03632; AAA49791.1; -
 DR PIR; B31933; B31933.
 DR HSSP; P01810; ZFBJ.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; Igv_1.
 DR Immunoglobulin V region; Signal.
 NON_TER 1 1
 FT SIGNAL 1 18 IG HEAVY CHAIN V REGION XIG14.
 FT CHAIN 19 135
 FT NON_TER 135 135
 SO SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;
 Query Match 49.8%; Score 315.5; DB 1; Length 135;
 Best Local Similarity 52.1%; Pred. No. 5,3e-25;
 Matches 62; Conservative 20; Mismatches 34; Indels 3; Gaps 2;
 QY 3 TLKESGPGILQPSQTLSTLCTSGFSLSTSGMGVSIKROPSGKGLMIAHYWDDDKRYN 62
 DB 20 TLQESGPGILVAPSSQSLTCTVSGFSLSTGYWIRPPGKGLMIGCVITYGSIY 77
 QY 63 PSLKSRITSKDTSNNOVFLKITSVDTRDTATYTCARVSLAYAMDYWGQTSVTYSS 121
 DB 78 DSLKRVITITDKNKKQVYLQMGMEVMDTATYTCAREYA-SGVNFDYWGQTVVTVTS 135
 RESULT 12
 HV60_MOUSE STANDARD; PRT; 116 AA.
 AC P18531;
 ID HV60_MOUSE
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region M315 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 PIR; J05059; HVMS31.

DR	HSSP: P01825; 7FAB.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	InterPro: IPR003596; Ig_V.	
DR	Pfam: PF00047; Ig: 1.	
DR	SMART: SM00406; IGV: 1.	
KW	Immunoglobulin V region; Signal.	
FT	SIGNAL	1
FT	CHAIN	18
FT	CHAIN	19
FT	DOMAIN	116
FT	DOMAIN	19
FT	DOMAIN	48
FT	DOMAIN	49
FT	DOMAIN	53
FT	DOMAIN	67
FT	DOMAIN	54
FT	DOMAIN	68
FT	DOMAIN	84
FT	DOMAIN	85
FT	DISULFID	116
FT	DISULFID	40
FT	NON_TER	114
FT	NON_TER	116
SO	SEQUENCE	116 AA; 13095 MW; 4562E03E55DC9E10 CRC64;

[illegible]

	RESULT	13		
ID	HV2I_HUMAN			
AC	P06331;	STANDARD;	PRT:	146 AA.
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JUN-1988 (Rel. 06, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V-II region ARH-77 precursor.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85205332; PubMed=3928255;			
RA	Kudo A., Ishihara T., Nishimura Y., Watanabe T.;			
RT	A cloned human immunoglobulin heavy chain gene with a novel direct repeat sequence in 5' flanking region.*;			
FT	Gene 33:181-189(1985).			
PR	A02101; G1HMZ2.			
DR	HSP: P01825; 7EAB.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_1.			
DR	SMART: SMO0406; IGV: 1.			
FW	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	19	
FT	CHAIN	20	146	IG HEAVY CHAIN V-II REGION ARH-77.
FT	DOMAIN	20	117	V SEGMENT.
FT	DOMAIN	118	127	D SEGMENT.
FT	DOMAIN	128	146	J SEGMENT.
FT	DISULEFID	42	115	BY SIMILARITY.
FT	NON_TER	146	146	
SQ	SEQUENCE	146 AA;	16228 MW;	807FD52BB218171F CRC64;

Query Match	48.9%	Score 309.5	DB 1	Length 146
Best Local Similarity	52.3%	Pred. No. 2.3e-24		
Matches 67, Conservative	14	Mismatches 38	Indels 9	Gaps 2

21 QVQLQDQMGAGLVKRPSETLSLTCAVEFGSGF--SGYIWSMIRQDPPRGLEIMGEININSGSTN 78

OY	6	YN	SL	SR	LT	IS	DS	NO	VF	LK	IT	SV	DP	AT	YV	CA	RV	SL	TA	-----	-Y	AM	Y	W	Q	113
		I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	:		I	I	I	I	
Db	79	YK	SL	SR	LT	IS	DS	NO	VF	LK	IT	SV	DP	AT	YV	CA	RV	SL	TA							
OY	114	GT	SV	TV	SS																					
		I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I							
Db	139	GI	TV	TV	SS																					
		I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I							

RESULT 14			
HV3K_HUMAN			
AC	HV3K_HUMAN	STANDARD:	PRT: 126 AA.
ID	P01772:		
DT	21-JUL-1986 (rel. 01, Created)		
DT	21-JUL-1986 (rel. 01, Last sequence update)		
DT	15-JUL-1999 (rel. 38, Last annotation update)		
DE	Ig heavy chain V-III region KOL.		
OS	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
OX	111		

RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE-83289131; PubMed-6684994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I." *Immunol.*
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).

RA 1.2-
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; Pubmed=7441755;
 RA Marquart M., Delsenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
 RT and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 DR PIR: A02055; G1HUKL.
 DR PDB: 2FB4; 12-JUL-89.
 DR PDB: 2IG2; 12-JUL-89.
 DR InterPro: IPR003506; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 KM SMART: SM00406; IGV; 1.
 RT Immunoglobulin V region; 3D-structure.
 RT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SEQ	NON_TER	126	126 AA;	1318 MM;	E4D71B52B16F8776 CRC64;
FT	DISULFID	105	110		
FT	STRAND	3	7		
FT	STRAND	11	12		
FT	TURN	14	15		
FT	STRAND	18	25		
FT	HELIX	29	31		
FT	STRAND	34	39		
FT	TURN	41	42		
FT	STRAND	46	51		
FT	TURN	53	54		
FT	STRAND	58	60		
FT	TURN	62	67		
FT	STRAND	68	73		
FT	TURN	74	77		
FT	STRAND	78	83		
FT	HELIX	88	90		
FT	STRAND	92	99		
FT	STRAND	106	106		
FT	TURN	107	108		
FT	STRAND	109	109		
FT	STRAND	113	113		
FT	STRAND	120	124		
FT	NON_TER	126	126		

Query Match 48.48; Score 306.5; DB 1; Length 126
Best Local Similarity 50.48; Pred. No. 3.9e-24;

	Query Match	Similarity	48.2%	Score 305	DB 1:	Length 117
	Best Local	Similarity	49.6%	Pred.	No. 5.1e-24	
	Matches	Conservative	24	Mismatches	33	Indels 4; Gaps 2
QY	1	QVTLKESGPGILQPSQTLSLTCSFSGFSLSITSGMGVSNIRPSPSGGLEMLAHIYWDDDKR	60			
Db	1	QVQLLEQSGPGIVLRPDSQTLSLTCFVGSGTFSSND-YVTWRQPPGRGLGEMIGVFYHGTS	58			
QY	61	YNPLSKSLKLTISKTSSNQVFLKITSVDTROTATYYCARRRSLTAAADYWGQGSVTVS	120			
Db	59	DTPPLRSRVLMVDTSKNQSFSLRLSSVTAADTAAYVCAR-NLLAGCIDVMWGGSGSLTVVS	116			
QY						
QY						
Db						

RESULT	15
ID	HVZG_HUMAN
AC	P01825;
STANDARD;	21-JUL-1986 (Rel. 01, Created)
PRT;	21-JUL-1986 (Rel. 01, last sequence update)
117 AA.	15-JUL-1999 (Rel. 38, last annotation update)
	Ig heavy chain V-II region NEMM.
	Homo sapiens (Human).
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
	NCBI_TaxID=9606;
	[1]
	SEQUENCE.
	MEDLINE-77242302; PubMed-407927;
	Pojtek R.J., Nakashima Y., Chen B.L., Konigsberg W.;
	"Amino acid sequence of the VH region of a human myeloma
	immunoglobulin (Ig New).";
	Biochemistry 16:3412-3420(1977).
	[2]
	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
	MEDLINE-78066916; PubMed-618887;
	Saul F.A., Amzel L.M., Poljak R.J.;
	"Preliminary refinement and structural analysis of the Fab fragment
	from human immunoglobulin new at 2.0-A resolution.";
	J. Biol. Chem. 253:585-597(1978).
	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG1 MYELOMA
	PROTEIN.
	PIR: A02100; GIHUMN.
	PDB: 7FAB; 31-JAN-94.
	InterPro: IPR003006; Ig_MHC.
	InterPro: IPR003596; Ig_V.
	Pfam: PF00047; Ig; 1.
	SMART: SM00406; IgV; 1.
	Immunoglobulin V region; 3D-structure.
	MOD_RS
	1 1 PIRROLIDONE CARBOXYLIC ACID.
	STRAND
	3 7
	FT STRAND
	11 12
	FT TURN
	14 15
	FT STRAND
	18 25
	FT TURN
	30 31
	FT STRAND
	33 39
	FT TURN
	41 42
	FT STRAND
	46 51
	FT TURN
	53 54
	FT STRAND
	57 59
	FT HELIX
	61 63
	FT TURN
	64 66
	FT SPRAND
	67 72
	FT TURN
	73 76
	FT STRAND
	77 82
	FT HELIX
	87 89
	FT STRAND
	91 98
	FT STRAND
	104 107
	FT STRAND
	111 115
	NON_TER
	117 117
	SEQUENCE
	117 AA; 12790 MW; 2DA47B509562D237 CRC64;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:34:22 ; Search time 79 Seconds
(Without alignments)
315.591 Million cell updates/sec

Title: US-09-759-112a-7
Perfect score: 633
Sequence: 1 QVTLKESGPGILQPSQTLSTL.....SLFAYADYWGQGSTVTVSS 121

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP virus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	471	74.4	121 4 Q9UL96	Q9UL96 homo sapien
2	398.5	63.0	121 11 Q99NG4	Q99NG4 mus musculu
3	370.5	58.5	482 11 Q91X92	Q91X92 mus musculu
4	361.5	57.1	496 4 Q96KX8	Q96KX8 homo sapien
5	361	57.0	119 4 Q9UL73	Q9UL73 homo sapien
6	356	56.2	97 4 Q43234	Q43234 homo sapien
7	354.5	56.0	613 4 Q96EY0	Q96EY0 homo sapien
8	343	54.2	479 11 Q99M22	Q99M22 mus musculu
9	341	53.9	588 4 Q8WU4	Q8WU4 mus sapien
10	341	53.9	597 4 Q9BU10	Q9BU10 homo sapien
11	341	53.9	618 4 Q96AA6	Q96AA6 homo sapien
12	338	53.4	597 4 Q9BOB8	Q9BOB8 homo sapien
13	337.5	53.3	150 4 Q95973	Q95973 homo sapien
14	331.5	52.4	122 4 Q9UL75	Q9UL75 homo sapien
15	305.5	48.3	147 4 Q9Y509	Q9Y509 homo sapien
16	302.5	47.8	613 4 Q8WU4	Q8WU4 homo sapien

17	301.5	47.6	473 4 Q8TC63	Q8TC63 homo sapien
18	295	46.6	113 4 Q9UL90	Q9UL90 homo sapien
19	288.5	45.6	112 4 Q9HC1	Q9HC1 homo sapien
20	284.5	44.9	573 4 Q8WU38	Q8WU38 homo sapien
21	284	44.9	116 4 Q9UL93	Q9UL93 homo sapien
22	278.5	44.0	122 4 Q9UL84	Q9UL84 homo sapien
23	276.5	43.7	473 11 Q91Z05	Q91Z05 mus musculu
24	273.5	43.2	118 4 Q9UL91	Q9UL91 homo sapien
25	272.5	43.0	118 4 Q9UL72	Q9UL72 homo sapien
26	272	43.0	121 4 Q9UL71	Q9UL71 homo sapien
27	272	43.0	131 4 Q9UL88	Q9UL88 homo sapien
28	269.5	42.6	145 11 Q924Q9	Q924Q9 mus musculu
29	269.5	42.6	471 4 Q8TC77	Q8TC77 homo sapien
30	269.5	42.6	484 11 Q8VEA0	Q8VEA0 mus musculu
31	268.5	42.4	298 11 Q9OYF0	Q9OYF0 mus musculu
32	268.5	42.1	145 11 Q924P7	Q924P7 mus musculu
33	265.5	41.9	487 11 Q99KX4	Q99KX4 mus musculu
34	264	41.7	597 4 Q96BB9	Q96BB9 homo sapien
35	263	41.5	468 11 Q99L31	Q99L31 mus musculu
36	262.5	41.5	494 4 Q96K68	Q96K68 homo sapien
37	261.5	41.3	145 11 Q924R1	Q924R1 mus musculu
38	261.5	41.3	469 11 Q8R3V9	Q8R3V9 mus musculu
39	260.5	41.2	145 11 Q924Q6	Q924Q6 mus musculu
40	259.5	41.0	241 11 Q921A6	Q921A6 mus musculu
41	257	40.6	484 11 Q99LA6	Q99LA6 mus musculu
42	256	40.4	118 4 Q9UL74	Q9UL74 homo sapien
43	255.5	40.4	145 11 Q924R4	Q924R4 mus musculu
44	255	40.3	119 11 Q920E7	Q920E7 mus musculu
45	254	40.1	146 11 Q924Q3	Q924Q3 mus musculu

ALIGNMENTS

RESULT 1

Q9UL96 PRELIMINARY; PRT; 121 AA.
ID Q9UL96
AC Q9UL96;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
DE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035018; AAD56254.1; -
DR HSSP: P01825; 7FAB;
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; Ig_v. 1.
FT NON_TER 1
FT NON_TER 121
SO SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CMC64;

Query Match 74.4%; Score 471; DB 4; Length 121;
Best Local Similarity 73.6%; Pred. No. 1.6e-44;
Matches 89; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

OY 1 QVTLKESGPGILQPSQTLSTLCSFGSLTSGMGVSHIROPSGKGLFALHIYWDK 60
DB 1 QVTLKESGPGILQPSQTLSTLCSFGSLTSGMGVSHIROPSGKGLFALHIYWDK 60

QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTSVTYS 120
DB 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTSVTYS 120
QY 121 S 121
DB 121 S 121

RESULT 2
Q99NG4 PRELIMINARY; PRT; 121 AA.
AC 099NG4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Plasmid PHEN1.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRATIN-BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawilisch H., Frank R., Hennecke M., Beensch M., Sohns B., Arseniev L.,
Bauteuch W., Kola A., Klos A., Koehl J.;
RT Site-directed C3a-Receptor Antibodies from Phage Display Libraries.;
RL J Immunol. 160:2947-2958(1998).
DR EMBL: AJ222590; CAI10890.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_Y.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_1like; 1.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 121 AA; 13255 MW; D293E4B8C5905B CRC64;

Query Match 63.0%; Score 398.5; DB 11; Length 121;
Best Local Similarity 64.8%; Pred. No. 1,7e-36;
Matches 79; Conservative 17; Mismatches 23; Indels 3; Gaps 2;

DB 1 QVTLKESGPGIILPQSOTLSLTCSEFSGFSLSTSGMGVSWIRPGSGKLEWLAHIYMDDDR 60
DB 1 QVTLKESGPGIILPQSOTLSLTCSEFSGFSLSTSGMGVSWIRPGSGKLEWLAHIYMDDDR 60
DB 1 QVTLKESGPGIILPQSOTLSLTCSEFSGFSLSTSGMGVSWIRPGSGKLEWLAHIYMDDDR 60
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTSVTYS 119
DB 59 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTSVTYS 118
QY 120 SS 121
DB 119 SS 120

RESULT 3
Q91X92 PRELIMINARY; PRT; 482 AA.
AC 091X92;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Unknown (protein for MGC:18822).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011181; AAH11181.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC753C CRC64;

Query Match 58.5%; Score 370.5; DB 11; Length 482;
Best Local Similarity 61.2%; Pred. No. 1,4e-32;
Matches 74; Conservative 17; Mismatches 27; Indels 3; Gaps 2;

QY 1 QVTLKESGPGIILPQSOTLSLTCSEFSGFSLSTSGMGVSWIRPGSGKLEWLAHIYMDDDR 60
DB 20 QVTLKESGPGIILPQSOTLSLTCSEFSGFSLSTSGMGVSWIRPGSGKLEWLAHIYMDDDR 77
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTSVTYS 120
DB 78 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTSVTYS 136
QY 121 S 121
DB 137 S 137

RESULT 4
Q96KX8 PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 53.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC016369; AAH16369.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 57.1%; Score 361.5; DB 4; Length 496;
Best Local Similarity 59.2%; Pred. No. 1,4e-31;
Matches 74; Conservative 17; Mismatches 29; Indels 5; Gaps 2;

QY 1 QVTLKESGPGIILPQSOTLSLTCSEFSGFSLSTSGMGVSWIRPGSGKLEWLAHIYMDDDR 60
DB 20 QVTLKESGPGIILPQSOTLSLTCSEFSGFSLSTSGMGVSWIRPGSGKLEWLAHIYMDDDR 79
QY 61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTS 116
DB 80 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYGCGTS 138
QY 117 VTYSS 121
DB 139 VTYSS 143

RESULT 5
Q9UL73 PRELIMINARY; PRT; 119 AA.

AC Q9UL73;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Myosin-reactive Immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035041; AAD56277.1; -.
 DR HSSP: P01825; 7FAB.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;

Query Match 57.0%; Score 361; DB 4; Length 119;
 Best Local Similarity 58.7%; Pred. No. 2,4e-32;
 Matches 71; Conservative 16; Mismatches 32; Indels 2; Gaps 1;

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGSGLEMLAHYWDKRR 60
 DB 1 QVQLQESGPGILQPSQTLSTLCTVSGFSLSTSGMGVSWIRQPSGSGLEMLAHYWDKRR 58
 OY 61 YNPSLKRSLTISKDTSSNOVFLKITSVDRATYTCARRVSLTAYAMDYWGQSTVTV 120
 DB 59 YTPSLKSRVTVISVDKSKNQFSLKLSLTAADTAYTCARRVSLTAYAMDYWGQSTVTV 118
 OY 121 S 121
 DB 119 S 119

RESULT 6
 ID 043234 PRELIMINARY; PRT; 97 AA.
 AC 043234;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Rheumatoid factor RF-ET13 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borrezen M., Natvig J.B., Thompson K.M.;
 RT "Heterogenous RF structures between and within healthy individuals are not related to HLA DRB1*0401".
 RL Mol. Immunol. 0:0-0(1997).
 DR EMBL: AF035802; AAB8534.1; -.
 DR HSSP: P01789; 1MCP.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT 97
 SQ SEQUENCE 97 AA; 10748 MW; DDC0BFA7B9AA812D CRC64;

Query Match 56.2%; Score 356; DB 4; Length 97;
 Best Local Similarity 68.0%; Pred. No. 6,6e-32;
 Matches 66; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

OY 3 TLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGSGLEMLAHYWDKRR 62
 DB 1 TLKESGPGILQPSQTLSTLCTVSGFSLSTSGMGVSWIRQPSGSGLEMLAHYWDKRR 60
 OY 63 PSLSKRLTISKDTSSNOVFLKITSVDRATYTCARRVSLTAYAMDYWGQSTVTV 99
 DB 61 TSLKSRSLTISKDTSSNOVFLKITSVDRATYTCARRVSLTAYAMDYWGQSTVTV 97

RESULT 7
 ID Q96EY0 PRELIMINARY; PRT; 613 AA.
 AC Q96EY0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Unknown (protein for MGC:20337).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-CELL;
 RA Strausberg R.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011857; AAH11857.1; -.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; 1g; 5.
 DR SMART: SM00408; 1GC2; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FE8421E7 CRC64;

Query Match 56.0%; Score 354.5; DB 4; Length 613;
 Best Local Similarity 59.0%; Pred. No. 1.1e-30;
 Matches 72; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

OY 1 QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVSWIRQPSGSGLEMLAHYWDKRR 60
 DB 20 QVQLQESGPGILQPSQTLSTLCTVSGFSLSTSGMGVSWIRQPSGSGLEMLAHYWDKRR 77
 OY 61 YNPSLKRSLTISKDTSSNOVFLKITSVDRATYTCARRVSLTAYAMDYWGQSTVTV 119
 DB 78 YNPSLKRSLTISKDTSSNOVFLKITSVDRATYTCARRVSLTAYAMDYWGQSTVTV 137
 OY 120 SS 121
 DB 138 SS 139

RESULT 8
 ID Q99M22 PRELIMINARY; PRT; 479 AA.
 AC Q99M22;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 52.0 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC002091; AAH02091.1; -.

DR EMBL: BC017356; AAH17356.1; -
 DR Interpro: IPR003598; Ig_C2.
 DR Interpro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00408; IgC2; 1.
 DR PROSITE: PS00290; Ig_MHC; UNKNOWN_3.
 KM Hypothetical protein; Immunoglobulin domain.
 SO SEQUENCE 618 AA; 67758 MW; 96DBD4C7C69E0A6 CRC64;

Query Match 53.98; Score 341; DB 4; Length 618;
 Best Local Similarity 55.98; Pred. No. 3.5e-29;
 Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

QY 1 QVTLKESGPGILDPSPOTSLTSCFSFSLSTSGMGVSWIRPOPSGKLEMLAHYWDKKR 60
 DB 20 QVQLQSGAGLILPSESLSLFCVYGGSF--SGYVSWIRPOPSGKLEMLAHYWDKKR 77
 QY 61 YNPSLKSRITISKDTSSNOVFLKITSVDTRDTATYTCARRSLTA-----YANDYWGOG 114
 DB 78 YNPSLKSRVITISVDTSKKQLSKLSSYNADTATYTCARRVITRASPOTDGRYGMVWGOG 137
 QY 115 TSVTVSS 121
 DB 138 TTVTVSS 144

RESULT 12
 Q9BOB8 PRELIMINARY; PRT; 597 AA.

AC Q9BOB8; 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Unknown (protein for MGC:1905) (protein for MGC:1228).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIMPH;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 EMBL: BC006180; AAH06180.1; -
 EMBL: BC001872; AAH01872.1; -
 HSSP: P01825; 7PAB
 DR Interpro: IPR003599; Ig.
 DR Interpro: IPR003597; Ig_c1.
 DR Interpro: IPR003600; Ig_1k.
 DR Interpro: IPR003006; Ig_MHC.
 DR Interpro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; IgC1; 4.
 DR SMART: SM00406; IgV; 1.
 DR SMART: SM00410; Ig_1k; 1.
 DR PROSITE: PS00290; Ig_MHC; UNKNOWN_3.
 SO SEQUENCE 597 AA; 65300 MW; 2DAFAD50A63758E1 CRC64;

Query Match 53.48; Score 338; DB 4; Length 597;
 Best Local Similarity 55.98; Pred. No. 7.3e-29;
 Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

QY 1 QVTLKESGPGILDPSPOTSLTSCFSFSLSTSGMGVSWIRPOPSGKLEMLAHYWDKKR 60
 DB 20 QVQLQSGAGLILPSESLSLFCVYGGSF--SGYVSWIRPOPSGKLEMLAHYWDKKR 77
 QY 61 YNPSLKSRITISKDTSSNOVFLKITSVDTRDTATYTCARRSLTA-----YANDYWGOG 114

DB 78 YNPSLKSRVITISVDTSKKQLSKLSSYNADTATYTCARRVITRASPOTDGRYGMVWGOG 137
 QY 115 TSVTVSS 121
 DB 138 TTVTVSS 144

RESULT 13
 Q95973 PRELIMINARY; PRT; 150 AA.

AC Q95973; 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE VH4 heavy chain variable region precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
 RT "Clonal proliferation of IgM-secreting B cell in the synovium of
 RT Behcet's patient with arthritis."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF103795; AAC79084.1; -
 DR HSSP: P01825; 7PAB.
 DR Interpro: IPR003006; Ig_MHC.
 DR Interpro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 >150
 FT NON_TER 150
 SO SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 53.38; Score 337.5; DB 4; Length 150;
 Best Local Similarity 55.48; Pred. No. 1.3e-29;
 Matches 67; Conservative 19; Mismatches 32; Indels 3; Gaps 1;

QY 1 QVTLKESGPGILDPSPOTSLTSCFSFSLSTSGMGVSWIRPOPSGKLEMLAHYWDKKR 60
 DB 20 QVQLQSGAGLILPSESLSLFCVYGGSF--SGYVSWIRPOPSGKLEMLAHYWDKKR 77
 QY 61 YNPSLKSRITISKDTSSNOVFLKITSVDTRDTATYTCARRSLTAAYMDYWGOGSTVTVS 120
 DB 80 YNPSLKSRVITISVDTSKKQLSKLSSYNADTATYTCARRVITRASPOTDGRYGMVWGOG 136
 QY 121 S 121
 DB 137 S 137

RESULT 14
 Q9UL75 PRELIMINARY; PRT; 122 AA.

AC Q9UL75; 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

